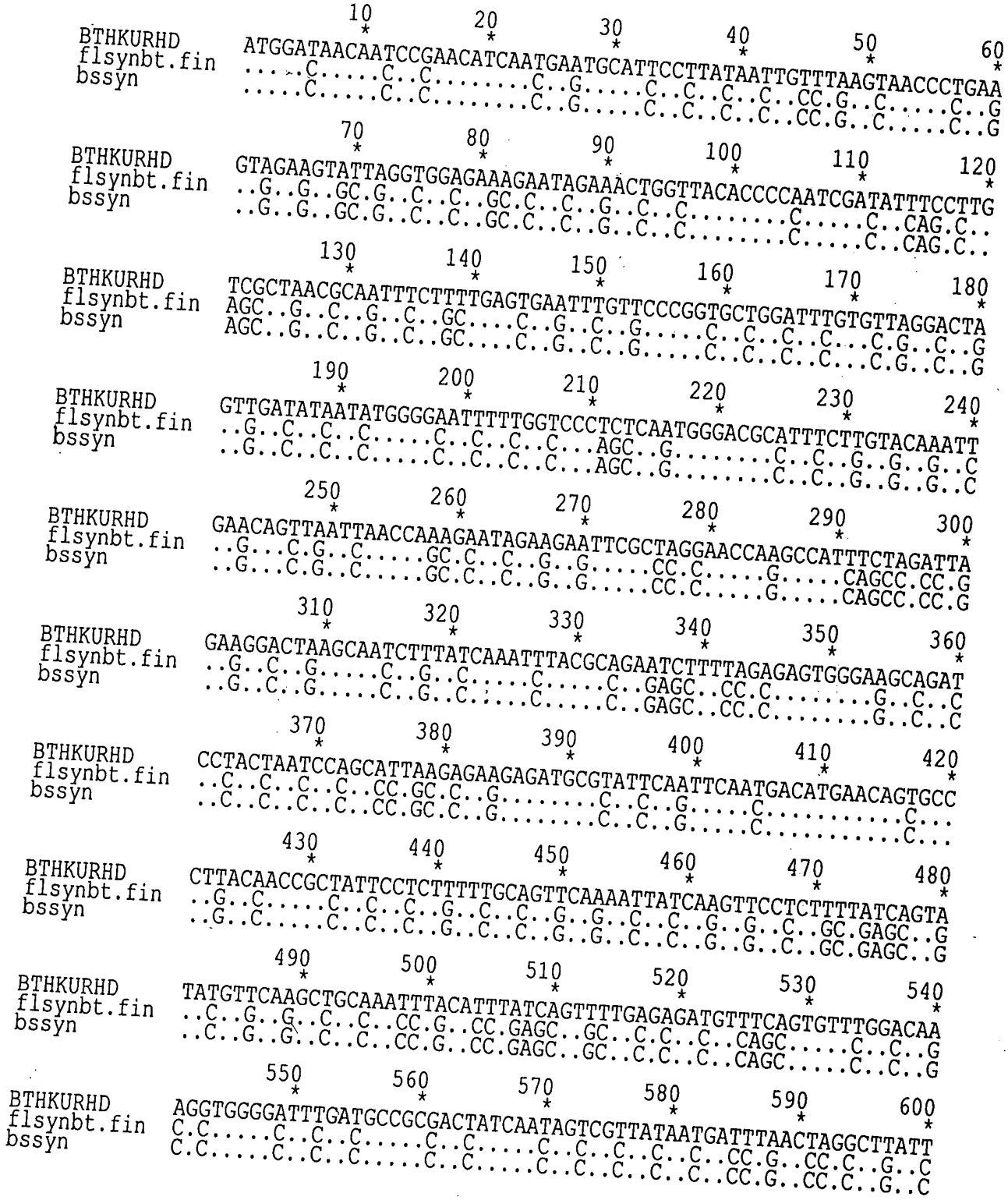
Fig. 1A



Docket #2988-960

Fig. 1B

```
                    610         620         630         640         650         660
                     *           *           *           *           *           *
BTHKURHD    GGCAACTATACAGATCATGCTGTACGCTGGTACAATACGGGATTAGAGCGTGTATGGGGA
flsynbt.fin ........C..C..C..C..C..G..........C..C..CC.G.....C..G.....T
bssyn       ........C..C..C..C..C..G..........C..C..CC.G.....C..G.....T

                    670         680         690         700         710         720
                     *           *           *           *           *           *
BTHKURHD    CCGGATTCTAGAGATTGGATAAGATATAATCAATTTAGAAGAGAATTAACACTAACTGTA
flsynbt.fin ..C..CAGCC.C..C.....C..G..C..C..G..CC.CC.C..GC.G..C..G..C..G
bssyn       ..C..CAGCC.C..C.....C..G..C..C..G..CC.CC.C..GC.G..C..G..C..G

                    730         740         750         760         770         780
                     *           *           *           *           *           *
BTHKURHD    TTAGATATCGTTTCTCTATTTCCGAACTATGATAGTAGAACGTATCCAATTCGAACAGTT
flsynbt.fin C.G..C.....GAGC..G..C..C.....C..C..CC.C..C..C..C..C..C..C..G
bssyn       C.G..C.....GAGC..G..C..C.....C..C..CC.C..C..C..C..C..C..C..G

                    790         800         810         820         830         840
                     *           *           *           *           *           *
BTHKURHD    TCCCAATTAACAAGAGAAATTTATACAAACCCAGTATTAGAAAATTTTGATGGTAGTTTT
flsynbt.fin AG...GC.G..CC.C..G.....C..C.....C..GC.G..G..C..C..C..C..C..C
bssyn       AG...GC.G..CC.C..G.....C..C.....C..GC.G..G..C..C..C..C..C..C

                    850         860         870         880         890         900
                     *           *           *           *           *           *
BTHKURHD    CGAGGCTCGGCTCAGGGCATAGAAGGAAGTATTAGGAGTCCACATTTGATGGATATACTT
flsynbt.fin ..C...AGC..C........C..G..C..C..CC.C..C..C..CC.......C..C..G
bssyn       ..C...AGC..C........C..G..C..C..CC.C..C..C..CC.......C..C..G

                    910         920         930         940         950         960
                     *           *           *           *           *           *
BTHKURHD    AACAGTATAACCATCTATACGGATGCTCATAGAGGAGAATATTATTGGTCAGGGCATCAA
flsynbt.fin .....C..C........C..C..C..C..CC.C..C..G..C..C...AGC..C..C..G
bssyn       .....C..C........C..C..C..C..CC.C..C..G..C..C...AGC..C..C..G

                    970         980         990         1000        1010        1020
                     *           *           *           *           *           *
BTHKURHD    ATAATGGCTTCTCCTGTAGGGTTTTCGGGGCCAGAATTCACTTTTCCGCTATATGGAACT
flsynbt.fin ..C.....CAGC..C..C..C..CAGC..C..C..G.....C..C..C..G..C..C..C
bssyn       ..C.....CAGC..C..C..C..CAGC..C..C..G.....C..C..C..G..C..C..C

                    1030        1040        1050        1060        1070        1080
                     *           *           *           *           *           *
BTHKURHD    ATGGGAAATGCAGCTCCACAACAACGTATTGTTGCTCAACTAGGTCAGGGCGTGTATAGA
flsynbt.fin .....C..C..T..A..T..G..G..C..C..G..A..G..G..C.....A.....CC.C
bssyn       .....C..C..T..A..T..G..G..C..C..G..A..G..G..C.....A.....CC.C

                    1090        1100        1110        1120        1130        1140
                     *           *           *           *           *           *
BTHKURHD    ACATTATCGTCCACTTTATATAGAAGACCTTTTAATATAGGGATAAATAATCAACAACTA
flsynbt.fin ..CC.GAGCAG...CC.G..CC.TC.......C..C..C..C..C..C..C..G..G..G
bssyn       ..CC.GAGCAG...CC.G..CC.TC.......C..C..C..C..C..C..C..G..G..G

                    1150        1160        1170        1180        1190        1200
                     *           *           *           *           *           *
BTHKURHD    TCTGTTCTTGACGGGACAGAATTTGCTTATGGAACCTCCTCAAATTTGCCATCCGCTGTA
flsynbt.fin AGC..G..G.....C..C..G..C..C..C..C...AG.AGC..CC....CAG...C..G
bssyn       AGC..G..G.....C..C..G..C..C..C..C...AG.AGC..CC....CAG...C..G
```

EP0274690A2 14-07-1988

Fig. 1C

```
                    1210       1220       1230       1240       1250       1260
                     *          *          *          *          *          *
BTHKURHD      TACAGAAAAAGCGGAACGGTAGATTCGCTGGATGAAATACCGCCACAGAATAACAACGTG
flsynbt.fin   ...C.C..G.....C..C..G..CAGC.....C..G..C..C..T.....C.........
bssyn         ...C.C..G.....C..C..G..CAGC.....C..G..C..C..T.....C.........

                    1270       1280       1290       1300       1310       1320
                     *          *          *          *          *          *
BTHKURHD      CCACCTAGGCAAGGATTTAGTCATCGATTAAGCCATGTTTCAATGTTTCGTTCAGGCTTT
flsynbt.fin   ......C.A..G..C..C..C..C..TC.G.....C..GAGC.....C..CAGT.....C
bssyn         ......C.A..G..C..C..C..C..TC.G.....C..GAGC.....C..CAGT.....C

                    1330       1340       1350       1360       1370       1380
                     *          *          *          *          *          *
BTHKURHD      AGTAATAGTAGTGTAAGTATAATAAGAGCTCCTATGTTCTCTTGGATACATCGTAGTGCT
flsynbt.fin   ..C..C..C..C..G..C..C..CC.T..A.........AGC.....T..C..C.....C
bssyn         ..C..C..C..C..G..C..C..CC.T..A.........AGC.....T..C..C.....C

                    1390       1400       1410       1420       1430
                     *          *          *          *          *
BTHKURHD      GAATTTAATAATATAATTCCTTCATCA--CAAATTACACAAATACCTTTAACAAAATCTA
flsynbt.fin   ..G..C..C..C..C..C..--..G..GC..G..C..C..G..C..CC.G..C..GAGC.
bssyn         ..G..C..C..C..C..C..--..G..GC..G..C..C..G..C..CC.G..C..GAGC.

               1440       1450       1460       1470       1480       1490
                *          *          *          *          *          *
BTHKURHD      CTAATCTTGGCTCTGGAACTTCTGTCGTTAAAGGACCAGGATTTACAGGAGGAGATATTC
flsynbt.fin   .C..C..G...AGC..C..CAGC..G..G..G..C..C..C..C..C..C..C..C..C.
bssyn         .C..C..G...AGC..C..CAGC..G..G..G..C..C..C..C..C..C..C..C..C.

               1500       1510       1520       1530       1540       1550
                *          *          *          *          *          *
BTHKURHD      TTCGAAGAACTTCACCTGGCCAGATTTCAACCTTAAGAGTAAATATTACTGCACCATTAT
flsynbt.fin   .G..CC.C..CAGC..C........CAGC...C.GC.C..G..C..C..C..C..CC.GA
bssyn         .G..CC.C..CAGC..C........CAGC...C.GC.C..G..C..C..C..C..CC.GA

               1560       1570       1580       1590       1600       1610
                *          *          *          *          *          *
BTHKURHD      CACAAAGATATCGGGTAAGAATTCGCTACGCTTCTACCACAAATTTACAATTCCATACAT
flsynbt.fin   GC..GC.C..C..C..CC.C..C........CAGC.....C..CC.G..G.....C..CA
bssyn         GC..GC.C..C..C..CC.C..C........CAGC.....C..CC.G..G.....C..CA

               1620       1630       1640       1650       1660       1670
                *          *          *          *          *          *
BTHKURHD      CAATTGACGGAAGACCTATTAATCAGGGGAATTTTTCAGCAACTATGAGTAGTGGGAGTA
flsynbt.fin   GC..C.....CC.C..C..C..C.....C..C..CAGC..C..C.....C..C..C..C.
bssyn         GC..C.....CC.C..C..C..C.....C..C..CAGC..C..C.....C..C..C..C.

               1680       1690       1700       1710       1720       1730
                *          *          *          *          *          *
BTHKURHD      ATTTACAGTCCGGAAGCTTTAGGACTGTAGGTTTTACTACTCCGTTTAACTTTTCAAATG
flsynbt.fin   .CC.G...AG...C.....CC.C..C..G..C..C..C..C..C..C.....CAGC..C.
bssyn         .CC.G...AG...C.....CC.C..C..G..C..C..C..C..C..C.....CAGC..C.

               1740       1750       1760       1770       1780       1790
                *          *          *          *          *          *
BTHKURHD      GATCAAGTGTATTTACGTTAAGTGCTCATGTCTTCAATTCAGGCAATGAAGTTTATATAG
flsynbt.fin   .CAGC..C..G..C..CC.G..C..C..C..G.....CAGC.....C..G..G..C..C.
bssyn         .CAGC..C..G..C..CC.G..C..C..C..G.....CAGC.....C..G..G..C..C.
```

09984624 - 112004

Fig. 1D

```
                1800       1810       1820       1830       1840       1850
                   *          *          *          *          *          *
BTHKURHD        ATCGAATTGAATTTGTTCCGGCAGAAGTAACCTTTGAGGCAGAATATGATTTAGAAAGAG
flsynbt.fin     .C..C..C..G..C..G..C..C..G..G.....C.....C..G..C..CC.G..G..G.
bssyn           .C..C..C..G..C..G..C..C..G..G.....C.....C..G..C..CC.G..G..G.

                1860       1870       1880       1890       1900       1910
                   *          *          *          *          *          *
BTHKURHD        CACAAAAGGCGGTGAATGAGCTGTTTACTTCTTCCAATCAAATCGGGTTAAAAACAGATG
flsynbt.fin     .T..G.....C.....C........C..CAGCAG...C..G.....CC.G..G..C..C.
bssyn           .T..G.....C.....C........C..CAGCAG...C..G.....CC.G..G..C..C.

                1920       1930       1940       1950       1960       1970
                   *          *          *          *          *          *
BTHKURHD        TGACGGATTATCATATTGATCAAGTATCCAATTTAGTTGAGTGTTTATCTGATGAATTTT
flsynbt.fin     ....C..C..C..C..C.....G..GAG...CC.G..G.....CC.GAGC..C..G..C.
bssyn           ....C..C..C..C..C....----------------------------------------

                1980       1990       2000       2010       2020       2030
                   *          *          *          *          *          *
BTHKURHD        GTCTGGATGAAAAAAAAGAATTGTCCGAGAAAGTCAAACATGCGAAGCGACTTAGTGATG
flsynbt.fin     .C.....C..G..G..G..GC..AG......G..G..G..C..C.....C..G..C..C.
bssyn           ----------------------------------------------------------

                2040       2050       2060       2070       2080       2090
                   *          *          *          *          *          *
BTHKURHD        AGCGGAATTTACTTCAAGATCCAAACTTTAGAGGGATCAATAGACAACTAGACCGTGGCT
flsynbt.fin     ....C..CC.G..G..G..C..C.....CC.C..C.....CC.C..G..G.....C....
bssyn           ----------------------------------------------------------

                2100       2110       2120       2130       2140       2150
                   *          *          *          *          *          *
BTHKURHD        GGAGAGGAAGTACGGATATTACCATCCAAGGAGGCGATGACGTATTCAAAGAGAATTACG
flsynbt.fin     ..C.C..C..C..C..C..C........G..C.....C.....G.....G.....C....
bssyn           ----------------------------------------------------------

                2160       2170       2180       2190       2200       2210
                   *          *          *          *          *          *
BTHKURHD        TTACGCTATTGGGTACCTTTGATGAGTGCTATCCAACGTATTTATATCAAAAAATAGATG
flsynbt.fin     .G..C..GC....C.....C..C........C..C..C..CC.G..C..G..G..C..C.
bssyn           ----------------------------------------------------------

                2220       2230       2240       2250       2260       2270
                   *          *          *          *          *          *
BTHKURHD        AGTCGAAATTAAAAGCCTATACCCGTTACCAATTAAGAGGGTATATCGAAGATAGTCAAG
flsynbt.fin     ..AGC..GC.G..G.....C.....C.....GC.GC.C..C..C.....G..C..C..G.
bssyn           ----------------------------------------------------------

                2280       2290       2300       2310       2320       2330
                   *          *          *          *          *          *
BTHKURHD        ACTTAGAAATCTATTTAATTCGCTACAATGCCAAACACGAAACAGTAAATGTGCCAGGTA
flsynbt.fin     ..C.G..G.....CC.G..C........C.....G.....G..C..G..C.....C..C.
bssyn           ----------------------------------------------------------

                2340       2350       2360       2370       2380       2390
                   *          *          *          *          *          *
BTHKURHD        CGGGTTCCTTATGGCCGCTTTCAGCCCCAAGTCCAATCGGAAAATGTGCCCATCATTCCC
flsynbt.fin     .C..CAG.C.G.....C..GAGC.....C..C..C.....C..G..C.....C..CAG..
bssyn           ----------------------------------------------------------
```

09884625 - 111200

Fig. 1E

```
                2400       2410       2420       2430       2440       2450
                 *          *          *          *          *          *
BTHKURHD        ATCATTTCTCCTTGGACATTGATGTTGGATGTACAGACTTAAATGAGGACTTAGGTGTAT
flsynbt.fin     .C..C...AG.C.......C..C..G..C..C..C...C.G..C......C.G..C..G.
bssyn           ------------------------------------------------------------

                2460       2470       2480       2490       2500       2510
                 *          *          *          *          *          *
BTHKURHD        GGGTGATATTCAAGATTAAGACGCAAGATGGCCATGCAAGACTAGGAAATCTAGAATTTC
flsynbt.fin     .......C........C.....C..G..C.....C..CC.C..G..C..C..G..G..C.
bssyn           ------------------------------------------------------------

                2520       2530       2540       2550       2560       2570
                 *          *          *          *          *          *
BTHKURHD        TCGAAGAGAAACCATTAGTAGGAGAAGCACTAGCTCGTGTGAAAAGAGCGGAGAAAAAAT
flsynbt.fin     .G..G.....G..CC.G..G..C..G..C..G..C..C.....GC.C..C.....G..G.
bssyn           ------------------------------------------------------------

                2580       2590       2600       2610       2620       2630
                 *          *          *          *          *          *
BTHKURHD        GGAGAGACAAACGTGAAAAATTGGAATGGGAAACAAATATTGTTTATAAAGAGGCAAAAG
flsynbt.fin     ..C.C.....G..C..G..GC....G.....G..C..C..C..G..C..G.....C..G.
bssyn           ------------------------------------------------------------

                2640       2650       2660       2670       2680       2690
                 *          *          *          *          *          *
BTHKURHD        AATCTGTAGATGCTTTATTTGTAAACTCTCAATATGATAGATTACAAGCGGATACCAACA
flsynbt.fin     .GAGC..G..C..CC.G..C..G...AGC..G..C..CC.CC.G..G..C..C.......
bssyn           ------------------------------------------------------------

                2700       2710       2720       2730       2740       2750
                 *          *          *          *          *          *
BTHKURHD        TCGCGATGATTCATGCGGCAGATAAACGCGTTCATAGCATTCGAGAAGCTTATCTGCCTG
flsynbt.fin     ....C.....C..C..C..C..C..G.....G..C........C..G..C..C.....C.
bssyn           ------------------------------------------------------------

                2760       2770       2780       2790       2800       2810
                 *          *          *          *          *          *
BTHKURHD        AGCTGTCTGTGATTCCGGGTGTCAATGCGGCTATTTTTGAAGAATTAGAAGGGCGTATTT
flsynbt.fin     .....AGC.....C..C..C..G..C..C..C..C..C..G..GC.G..G..C..C..C.
bssyn           ------------------------------------------------------------

                2820       2830       2840       2850       2860       2870
                 *          *          *          *          *          *
BTHKURHD        TCACTGCATTCTCCCTATATGATGCGAGAAATGTCATTAAAAATGGTGATTTTAATAATG
flsynbt.fin     ....C..C...AG...G..C..C..CC.C..C..G..C..G..C..C..C..C..C..C.
bssyn           ------------------------------------------------------------

                2880       2890       2900       2910       2920       2930
                 *          *          *          *          *          *
BTHKURHD        GCTTATCCTGCTGGAACGTGAAAGGGCATGTAGATGTAGAAGAACAAAACAACCACCGTT
flsynbt.fin     ..C.GAG..............G..C..C..G..C..G..G..G..G...........CA
bssyn           ------------------------------------------------------------

                2940       2950       2960       2970       2980       2990
                 *          *          *          *          *          *
BTHKURHD        CGGTCCTTGTTGTTCCGGAATGGGAAGCAGAAGTGTCACAAGAAGTTCGTGTCTGTCCGG
flsynbt.fin     GC..G..G..G..G..C..G.....G..C..G...AGC..G..G..G..C..G..C..C.
bssyn           ------------------------------------------------------------
```

09988452 - 141204

Fig. 1F

```
                3000       3010       3020       3030       3040       3050
                 *          *          *          *          *          *
BTHKURHD        GTCGTGGCTATATCCTTCGTGTCACAGCGTACAAGGAGGGATATGGAGAAGGTTGCGTAA
flsynbt.fin     .C..C.....C.....G..C..G..C..C..........C..C..C..G..C.....G.
bssyn           ------------------------------------------------------------

                3060       3070       3080       3090       3100       3110
                 *          *          *          *          *          *
BTHKURHD        CCATTCATGAGATCGAGAACAATACAGACGAACTGAAGTTTAGCAACTGTGTAGAAGAGG
flsynbt.fin     ....C..C.............C..C.....G..C.....C........C..G..G....
bssyn           ------------------------------------------------------------

                3120       3130       3140       3150       3160       3170
                 *          *          *          *          *          *
BTHKURHD        AAGTATATCCAAACAACACGGTAACGTGTAATGATTATACTGCGACTCAAGAAGAATATG
flsynbt.fin     .G..G..C..C........C..G..C..C..C..C..C..C..C..G..G..G..C.
bssyn           ------------------------------------------------------------

                3180       3190       3200       3210       3220       3230
                 *          *          *          *          *          *
BTHKURHD        AGGGTACGTACACTTCTCGTAATCGAGGATATGACGGAGCCTATGAAAGCAATTCTTCTG
flsynbt.fin     ....C..C.....CAGC..C..C..C..C..C.....C.....C..G.....CAGCAGC.
bssyn           ------------------------------------------------------------

                3240       3250       3260       3270       3280       3290
                 *          *          *          *          *          *
BTHKURHD        TACCAGCTGATTATGCATCAGCCTATGAAGAAAAAGCATATACAGATGGACGAAGAGACA
flsynbt.fin     .G..C..C..C..C..CAGC.....C..G..G..G..C..C..C..C..C..CC.C....
bssyn           ------------------------------------------------------------

                3300       3310       3320       3330       3340       3350
                 *          *          *          *          *          *
BTHKURHD        ATCCTTGTGAATCTAACAGAGGATATGGGGATTACACACCACTACCAGCTGGCTATGTGA
flsynbt.fin     .C..C..C..GAGC...C.C..C..C..C..C.....C..C..G..C..C.....C....
bssyn           ------------------------------------------------------------

                3360       3370       3380       3390       3400       3410
                 *          *          *          *          *          *
BTHKURHD        CAAAAGAATTAGAGTACTTCCCAGAAACCGATAAGGTATGGATTGAGATCGGAGAAACGG
flsynbt.fin     .C..G..GC.G..........C..G.....C.....G.....C........C..G..C.
bssyn           ------------------------------------------------------------

                3420       3430       3440       3450       3460
                 *          *          *          *          *
BTHKURHD        AAGGAACATTCATCGTGGACAGCGTGGAATTACTTCTTATGGAGGAATAA
flsynbt.fin     .G..C..C.....................GC.G..G..G........G..G
bssyn           ----------------------------------------...TG..G
```

EP 0 358 569 A2

Fig. 2A

```
                10        20        30        40        50        60
                *         *         *         *         *         *
BTHKURHD        ATGGATAACAATCCGAACATCAATGAATGCATTCCTTATAATTGTTTAAGTAACCCTGAA
bssyn           .....C.....C..C........C..G.....C..C..C..C..CC.G..C.....C..G

                70        80        90        100       110       120
                *         *         *         *         *         *
BTHKURHD        GTAGAAGTATTAGGTGGAGAAAGAATAGAAACTGGTTACACCCCAATCGATATTTCCTTG
bssyn           ..G..G..GC.G..C..C..GC.C..C..G..C..C........C.....C..CAG.C..

                130       140       150       160       170       180
                *         *         *         *         *         *
BTHKURHD        TCGCTAACGCAATTTCTTTTGAGTGAATTTGTTCCCGGTGCTGGATTTGTGTTAGGACTA
bssyn           AGC..G..C..G..C..GC....C..G..C..G.....C..C..C..C...C.G..C..G

                190       200       210       220       230       240
                *         *         *         *         *         *
BTHKURHD        GTTGATATAATATGGGGAATTTTTGGTCCCTCTCAATGGGACGCATTTCTTGTACAAATT
bssyn           ..G..C..C..C.....C..C..C..C...AGC..G........C..C..G..G..G..C

                250       260       270       280       290       300
                *         *         *         *         *         *
BTHKURHD        GAACAGTTAATTAACCAAAGAATAGAAGAATTCGCTAGGAACCAAGCCATTTCTAGATTA
bssyn           ..G...C.G..C.....GC.C..C..G..G.....CC.C.....G.....CAGCC.CC.G

                310       320       330       340       350       360
                *         *         *         *         *         *
BTHKURHD        GAAGGACTAAGCAATCTTTATCAAATTTACGCAGAATCTTTTAGAGAGTGGGAAGCAGAT
bssyn           ..G..C..G.....C..G..C.....C.....C..GAGC..CC.C........G..C..C

                370       380       390       400       410       420
                *         *         *         *         *         *
BTHKURHD        CCTACTAATCCAGCATTAAGAGAAGAGATGCGTATTCAATTCAATGACATGAACAGTGCC
bssyn           ..C..C..C..C..CC.GC.C..G........C..C..G.....C...........C...

                430       440       450       460       470       480
                *         *         *         *         *         *
BTHKURHD        CTTACAACCGCTATTCCTCTTTTTGCAGTTCAAAATTATCAAGTTCCTCTTTTATCAGTA
bssyn           ..G..C.....C..C..C..G..C..C..G..G..C..C..G..G..C..GC.GAGC..G

                490       500       510       520       530       540
                *         *         *         *         *         *
BTHKURHD        TATGTTCAAGCTGCAAATTTACATTTATCAGTTTTGAGAGATGTTTCAGTGTTTGGACAA
bssyn           ..C..G..G..C..C..CC.G..CC.GAGC..GC..C.C..C..CAGC.....C..C..G

                550       560       570       580       590       600
                *         *         *         *         *         *
BTHKURHD        AGGTGGGGATTTGATGCCGCGACTATCAATAGTCGTTATAATGATTTAACTAGGCTTATT
bssyn           C.C.....C..C..C.....C..C.....C..C..C..C..C..CC.G..CC.C..G..C

                610       620       630       640       650       660
                *         *         *         *         *         *
BTHKURHD        GGCAACTATACAGATCATGCTGTACGCTGGTACAATACGGGATTAGAGCGTGTATGGGGA
bssyn           ........C..C..C..C..C..G..........C..C..CC.G.....C..G.....T

                670       680       690       700       710       720
                *         *         *         *         *         *
BTHKURHD        CCGGATTCTAGAGATTGGATAAGATATAATCAATTTAGAAGAGAATTAACACTAACTGTA
bssyn           ..C..CAGCC.C..C.....C..G..C..C..G..CC.CC.C..GC.G..C..G..C..G
```

EP 0 274 260 A2

Fig. 2B

```
                730       740       750       760       770       780
                *         *         *         *         *         *
BTHKURHD        TTAGATATCGTTTCTCTATTTCCGAACTATGATAGTAGAACGTATCCAATTCGAACAGTT
bssyn           C.G..C.....GAGC..G..C..C.....C..C..CC.C..C..C..C..C..C..C..G

                790       800       810       820       830       840
                *         *         *         *         *         *
BTHKURHD        TCCCAATTAACAAGAGAAATTTATACAAACCCAGTATTAGAAAATTTTGATGGTAGTTTT
bssyn           AG...GC.G..CC.C..G.....C..C.....C..GC.G..G..C..C..C..C..C..C

                850       860       870       880       890       900
                *         *         *         *         *         *
BTHKURHD        CGAGGCTCGGCTCAGGGCATAGAAGGAAGTATTAGGAGTCCACATTTGATGGATATACTT
bssyn           ..C...AGC..C........C..G..C..C..CC.C..C..C..CC.......C..C..G

                910       920       930       940       950       960
                *         *         *         *         *         *
BTHKURHD        AACAGTATAACCATCTATACGGATGCTCATAGAGGAGAATATTATTGGTCAGGGCATCAA
bssyn           .....C..C........C..C..C..C..CC.C..C..G..C..C...AGC..C..C..G

                970       980       990       1000      1010      1020
                *         *         *         *         *         *
BTHKURHD        ATAATGGCTTCTCCTGTAGGGTTTTCGGGGCCAGAATTCACTTTTCCGCTATATGGAACT
bssyn           ..C.....CAGC..C..C..C..CAGC..C..C..G.....C..C..C..G..C..C..C

                1030      1040      1050      1060      1070      1080
                *         *         *         *         *         *
BTHKURHD        ATGGGAAATGCAGCTCCACAACAACGTATTGTTGCTCAACTAGGTCAGGGCGTGTATAGA
bssyn           .....C..C..T..A..T..G..G..C..C..G..A..G..G..C.....A.....CC.C

                1090      1100      1110      1120      1130      1140
                *         *         *         *         *         *
BTHKURHD        ACATTATCGTCCACTTTATATAGAAGACCTTTTAATATAGGGATAAATAATCAACAACTA
bssyn           ..CC.GAGCAG...CC.G..CC.TC.......C..C..C..C..C..C..C..G..G..G

                1150      1160      1170      1180      1190      1200
                *         *         *         *         *         *
BTHKURHD        TCTGTTCTTGACGGGACAGAATTTGCTTATGGAACCTCCTCAAATTTGCCATCCGCTGTA
bssyn           AGC..G..G.....C..C..G..C..C..C..C...AG.AGC..CC....CAG...C..G

                1210      1220      1230      1240      1250      1260
                *         *         *         *         *         *
BTHKURHD        TACAGAAAAAGCGGAACGGTAGATTCGCTGGATGAAATACCGCCACAGAATAACAACGTG
bssyn           ...C.C..G.....C..C..G..CAGC.....C..G..C..C..T.....C.........

                1270      1280      1290      1300      1310      1320
                *         *         *         *         *         *
BTHKURHD        CCACCTAGGCAAGGATTTAGTCATCGATTAAGCCATGTTTCAATGTTTCGTTCAGGCTTT
bssyn           ......C.A..G..C..C..C..C..TC.G.....C..GAGC.....C..CAGT.....C

                1330      1340      1350      1360      1370      1380
                *         *         *         *         *         *
BTHKURHD        AGTAATAGTAGTGTAAGTATAATAAGAGCTCCTATGTTCTCTTGGATACATCGTAGTGCT
bssyn           ..C..C..C..C..G..C..C..CC.T..A.........AGC.....T..C..C.....C

                1390      1400      1410      1420      1430
                *         *         *         *         *
BTHKURHD        GAATTTAATAATATAATTCCTTCATCA--CAAATTACACAAATACCTTTAACAAAATCTA
bssyn           ..G..C..C..C..C..C..--..G..GC..G..C..C..G..C..CC.G..C..GAGC.
```

09684452 - 112004

Fig. 2C

```
                1440        1450        1460        1470        1480        1490
                  *           *           *           *           *           *
BTHKURHD          CTAATCTTGGCTCTGGAACTTCTGTCGTTAAAGGACCAGGATTTACAGGAGGAGATATTC
bssyn             .C..C..G...AGC..C..CAGC..G..G..G..C..C..C..C..C..C..C..C..C.

                1500        1510        1520        1530        1540        1550
                  *           *           *           *           *           *
BTHKURHD          TTCGAAGAACTTCACCTGGCCAGATTTCAACCTTAAGAGTAAATATTACTGCACCATTAT
bssyn             .G..CC.C..CAGC..C........CAGC...C.GC.C..G..C..C..C..CC.GA

                1560        1570        1580        1590        1600        1610
                  *           *           *           *           *           *
BTHKURHD          CACAAAGATATCGGGTAAGAATTCGCTACGCTTCTACCACAAATTTACAATTCCATACAT
bssyn             GC..GC.C..C..C..CC.C..C........CAGC.....C..CC.G..G.....C..CA

                1620        1630        1640        1650        1660        1670
                  *           *           *           *           *           *
BTHKURHD          CAATTGACGGAAGACCTATTAATCAGGGGAATTTTTCAGCAACTATGAGTAGTGGGAGTA
bssyn             GC..C.....CC.C..C..C..C.....C..C..CAGC..C..C.....C..C..C..C.

                1680        1690        1700        1710        1720        1730
                  *           *           *           *           *           *
BTHKURHD          ATTTACAGTCCGGAAGCTTTAGGACTGTAGGTTTTACTACTCCGTTTAACTTTTCAAATG
bssyn             .CC.G...AG...C.....CC.C..C..G..C..C..C..C..C..C.....CAGC..C.

                1740        1750        1760        1770        1780        1790
                  *           *           *           *           *           *
BTHKURHD          GATCAAGTGTATTTACGTTAAGTGCTCATGTCTTCAATTCAGGCAATGAAGTTTATATAG
bssyn             .CAGC..C..G..C..CC.G..C..C..C..G.....CAGC.....C..G..G..C..C.

                1800        1810        1820        1830        1840        1850
                  *           *           *           *           *           *
BTHKURHD          ATCGAATTGAATTTGTTCCGGCAGAAGTAACCTTTGAGGCAGAATATGATTTAGAAAGAG
bssyn             .C..C..C..G..C..G..C..C..G..G.....C.....C..G..C..CC.G..G..G.

                1860        1870        1880        1890        1900        1910
                  *           *           *           *           *           *
BTHKURHD          CACAAAAGGCGGTGAATGAGCTGTTTACTTCTTCCAATCAAATCGGGTTAAAAACAGATG
bssyn             .T..G.....C.....C........C..CAGCAG...C..G.....CC.G..G..C..C.

                1920        1930        1940
                  *           *           *
BTHKURHD          TGACGGATTATCATATTGATCAAGTATCC
bssyn             ....C..C..C..C.....G..G.AG
```

Docket No. 4250-4

Fig. 3A

```
                    10        20        30        40        50        60
                    *         *         *         *         *         *
syn1T.mze   ATGGACAACAACCCCAACATCAACGAGTGCATCCCCTACAACTGCCTGAGCAACCCCGAG
bssyn       ............................................................
synful.mod  ............................................................

                    70        80        90       100       110       120
                    *         *         *         *         *         *
syn1T.mze   GTGGAGGTGCTGGGCGGCGAGCGCATCGAGACCGGCTACACCCCCATCGACATCAGCCTG
bssyn       ............................................................
synful.mod  ............................................................

                   130       140       150       160       170       180
                    *         *         *         *         *         *
syn1T.mze   AGCCTGACCCAGTTCCTGCTGAGCGAGTTCGTGCCCGGCGCCGGCTTCGTGCTGGGCCTG
bssyn       ............................................................
synful.mod  ............................................................

                   190       200       210       220       230       240
                    *         *         *         *         *         *
syn1T.mze   GTGGACATCATCTGGGGCATCTTCGGCCCCAGCCAGTGGGACGCCTTCCTGGTGCAGATC
bssyn       ............................................................
synful.mod  ............................................................

                   250       260       270       280       290       300
                    *         *         *         *         *         *
syn1T.mze   GAGCAGCTGATCAACCAGCGCATCGAGGAGTTCGCCCGCAACCAGGCCATCAGCCGCCTG
bssyn       ............................................................
synful.mod  ............................................................

                   310       320       330       340       350       360
                    *         *         *         *         *         *
syn1T.mze   GAGGGCCTGAGCAACCTGTACCAGATCTACGCCGAGAGCTTCCGCGAGTGGGAGGCCGAC
bssyn       ......................A.....................................
synful.mod  ......................A.....................................

                   370       380       390       400       410       420
                    *         *         *         *         *         *
syn1T.mze   CCCACCAACCCCGCCCTGCGCGAGGAGATGCGCATCCAGTTCAACGACATGAACAGCGCC
bssyn       ............................................................
synful.mod  ............................................................

                   430       440       450       460       470       480
                    *         *         *         *         *         *
syn1T.mze   CTGACCACCGCCATCCCCCTGTTCGCCGTGCAGAACTACCAGGTGCCCCTGCTGAGCGTG
bssyn       ............................................................
synful.mod  ............................................................

                   490       500       510       520       530       540
                    *         *         *         *         *         *
syn1T.mze   TACGTGCAGGCCGCCAACCTGCACCTGAGCGTGCTGCGCGACGTGAGCGTGTTCGGCCAG
bssyn       ..........................................C.................
synful.mod  ..........................................C.................

                   550       560       570       580       590       600
                    *         *         *         *         *         *
syn1T.mze   CGCTGGGGCTTCGACGCCGCCACCATCAACAGCCGCTACAACGACCTGACCCGCCTGATC
bssyn       ............................................................
synful.mod  ............................................................
```

US 6,248,540 B1

Fig. 3B

```
                    610        620        630        640        650        660
                     *          *          *          *          *          *
syn1T.mze    GGCAACTACACCGACCACGCCGTGCGCTGGTACAACACCGGCCTGGAGCGCGTGTGGGGC
bssyn        ..............................................................T
synful.mod   ..............................................................T

                    670        680        690        700        710        720
                     *          *          *          *          *          *
syn1T.mze    CCCGACAGCCGCGACTGGATCCGCTACAACCAGTTCCGCCGCGAGCTGACCCTGACCGTG
bssyn        ......................A.G.....................................
synful.mod   ......................A.G.....................................

                    730        740        750        760        770        780
                     *          *          *          *          *          *
syn1T.mze    CTGGACATCGTGAGCCTGTTCCCCAACTACGACAGCCGCACCTACCCCATCCGCACCGTG
bssyn        ..............................................................
synful.mod   ..............................................................

                    790        800        810        820        830        840
                     *          *          *          *          *          *
syn1T.mze    AGCCAGCTGACCCGCGAGATCTACACCAACCCCGTGCTGGAGAACTTCGACGGCAGCTTC
bssyn        ......................T.....................................
synful.mod   ......................T.....................................

                    850        860        870        880        890        900
                     *          *          *          *          *          *
syn1T.mze    CGCGGCAGCGCCCAGGGCATCGAGGGCAGCATCCGCAGCCCCCACCTGATGGACATCCTG
bssyn        ..............................................................
synful.mod   ..............................................................

                    910        920        930        940        950        960
                     *          *          *          *          *          *
syn1T.mze    AACAGCATCACCATCTACACCGACGCCCACCGCGGCGAGTACTACTGGAGCGGCCACCAG
bssyn        ..............................................................
synful.mod   ..............................................................

                    970        980        990       1000       1010       1020
                     *          *          *          *          *          *
syn1T.mze    ATCATGGCCAGCCCCGTGGGCTTCAGCGGCCCCGAGTTCACCTTCCCCCTGTACGGCACC
bssyn        ..................C...........................................
synful.mod   ..................C...........................................

                   1030       1040       1050       1060       1070       1080
                     *          *          *          *          *          *
syn1T.mze    ATGGGCAACGCCGCCCCCCAGCAGCGCATCGTGGCCCAGCTGGGCCAGGGCGTGTACCGC
bssyn        ...........T..A..T.................A..............A.........
synful.mod   ...........T..A..T.................A..............A.........

                   1090       1100       1110       1120       1130       1140
                     *          *          *          *          *          *
syn1T.mze    ACCCTGAGCAGCACCCTGTACCGCCGCCCCTTCAACATCGGCATCAACAACCAGCAGCTG
bssyn        ......................T..A..T...................................
synful.mod   ......................T..A..T...................................

                   1150       1160       1170       1180       1190       1200
                     *          *          *          *          *          *
syn1T.mze    AGCGTGCTGGACGGCACCGAGTTCGCCTACGGCACCAGCAGCAACCTGCCCAGCGCCGTG
bssyn        ..............................................................
synful.mod   ..............................................................
```

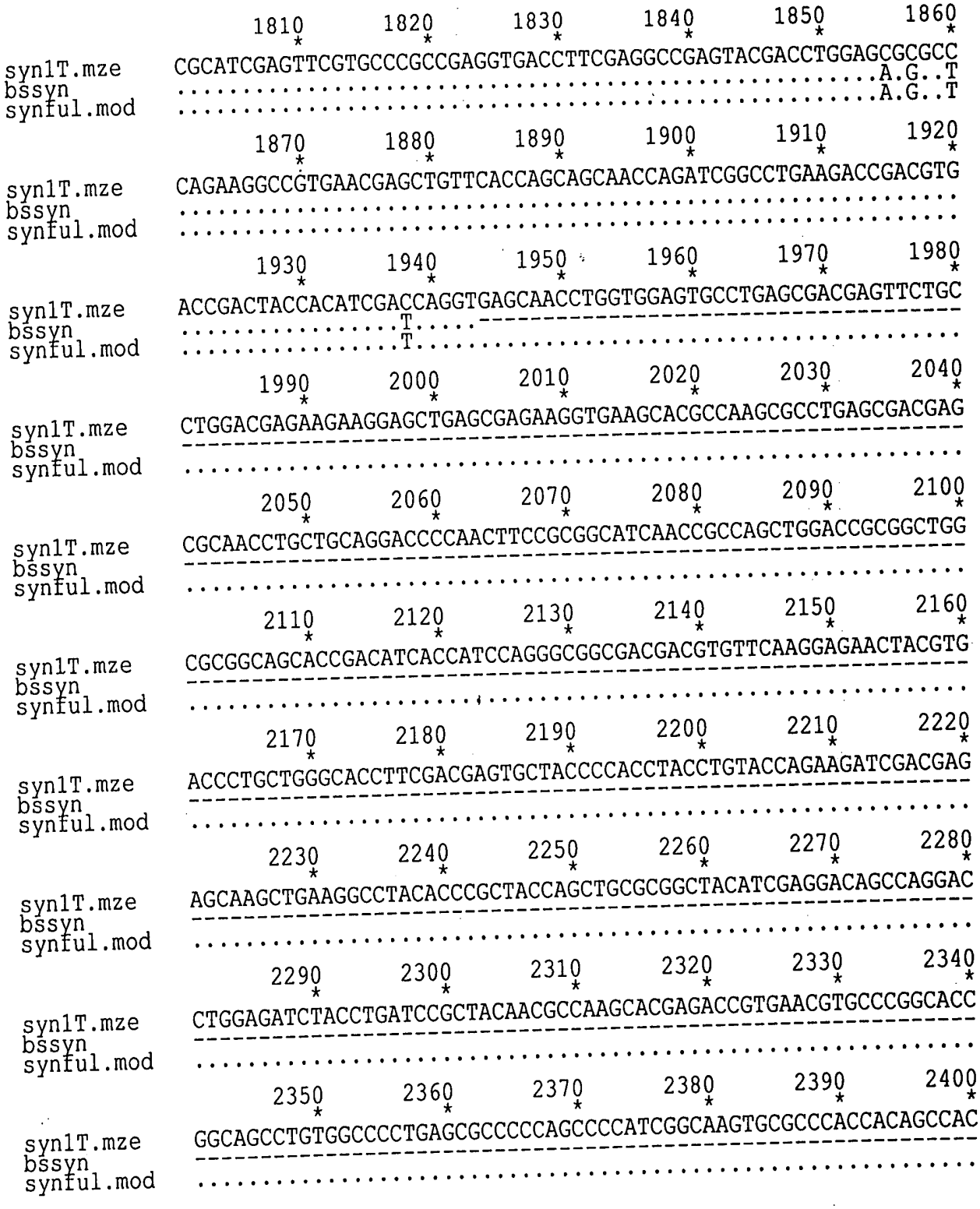
0698462 - 112004

Fig. 3C

```
                    1210       1220       1230       1240       1250       1260
                     *          *          *          *          *          *
syn1T.mze    TACCGCAAGAGCGGCACCGTGGACAGCCTGGACGAGATCCCCCCCCAGAACAACAACGTG
bssyn        ....................................................T.............
synful.mod   ....................................................T.............

                    1270       1280       1290       1300       1310       1320
                     *          *          *          *          *          *
syn1T.mze    CCCCCCCGCCAGGGCTTCAGCCACCGCCTGAGCCACGTGAGCATGTTCCGCAGCGGCTTC
bssyn        ..A..T..A.................T.........................T......
synful.mod   ..A..T..A.................T.........................T......

                    1330       1340       1350       1360       1370       1380
                     *          *          *          *          *          *
syn1T.mze    AGCAACAGCAGCGTGAGCATCATCCGCGCCCCCATGTTCAGCTGGATCCACCGCAGCGCC
bssyn        ........................T..A..T.............T........T...
synful.mod   ........................T..A..T.............T........T...

                    1390       1400       1410       1420       1430       1440
                     *          *          *          *          *          *
syn1T.mze    GAGTTCAACAACATCATCCCCAGCAGCCAGATCACCCAGATCCCCCTGACCAAGAGCACC
bssyn        ............................................................
synful.mod   ............................................................

                    1450       1460       1470       1480       1490       1500
                     *          *          *          *          *          *
syn1T.mze    AACCTGGGCAGCGGCACCAGCGTGGTGAAGGGCCCCGGCTTCACCGGCGGCGACATCCTG
bssyn        ............................................................
synful.mod   ............................................................

                    1510       1520       1530       1540       1550       1560
                     *          *          *          *          *          *
syn1T.mze    CGCCGCACCAGCCCCGGCCAGATCAGCACCCTGCGCGTGAACATCACCGCCCCCCTGAGC
bssyn        ............................................................
synful.mod   ............................................................

                    1570       1580       1590       1600       1610       1620
                     *          *          *          *          *          *
syn1T.mze    CAGCGCTACCGCGTGCGCATCCGCTACGCCAGCACCACCAACCTGCAGTTCCACACCAGC
bssyn        ..............C.............................................
synful.mod   ..............C.............................................

                    1630       1640       1650       1660       1670       1680
                     *          *          *          *          *          *
syn1T.mze    ATCGACGGCCGCCCCATCAACCAGGGCAACTTCAGCGCCACCATGAGCAGCGGCAGCAAC
bssyn        ............................................................
synful.mod   ............................................................

                    1690       1700       1710       1720       1730       1740
                     *          *          *          *          *          *
syn1T.mze    CTGCAGAGCGGCAGCTTCCGCACCGTGGGCTTCACCACCCCCTTCAACTTCAGCAACGGC
bssyn        ............................................................
synful.mod   ............................................................

                    1750       1760       1770       1780       1790       1800
                     *          *          *          *          *          *
syn1T.mze    AGCAGCGTGTTCACCCTGAGCGCCCACGTGTTCAACAGCGGCAACGAGGTGTACATCGAC
bssyn        ............................................................
synful.mod   ............................................................
```

09696470 - 112004

Fig. 3D



Docket: 2-1-0-0-0

Fig. 3E

```
                    2410       2420       2430       2440       2450       2460
                     *          *          *          *          *          *
syn1T.mze    CACTTCAGCCTGGACATCGACGTGGGCTGCACCGACCTGAACGAGGACCTGGGCGTGTGG
bssyn        ------------------------------------------------------------
synful.mod   ............................................................

                    2470       2480       2490       2500       2510       2520
                     *          *          *          *          *          *
syn1T.mze    GTGATCTTCAAGATCAAGACCCAGGACGGCCACGCCCGCCTGGGCAACCTGGAGTTCCTG
bssyn        ------------------------------------------------------------
synful.mod   ............................................................

                    2530       2540       2550       2560       2570       2580
                     *          *          *          *          *          *
syn1T.mze    GAGGAGAAGCCCCTGGTGGGCGAGGCCCTGGCCCGCGTGAAGCGCGCCGAGAAGAAGTGG
bssyn        ------------------------------------------------------------
synful.mod   ............................................................

                    2590       2600       2610       2620       2630       2640
                     *          *          *          *          *          *
syn1T.mze    CGCGACAAGCGCGAGAAGCTGGAGTGGGAGACCAACATCGTGTACAAGGAGGCCAAGGAG
bssyn        ------------------------------------------------------------
synful.mod   ............................................................

                    2650       2660       2670       2680       2690       2700
                     *          *          *          *          *          *
syn1T.mze    AGCGTGGACGCCCTGTTCGTGAACAGCCAGTACGACCGCCTGCAGGCCGACACCAACATC
bssyn        ------------------------------------------------------------
synful.mod   ............................................................

                    2710       2720       2730       2740       2750       2760
                     *          *          *          *          *          *
syn1T.mze    GCCATGATCCACGCCGCCGACAAGCGCGTGCACAGCATCCGCGAGGCCTACCTGCCCGAG
bssyn        ------------------------------------------------------------
synful.mod   ........................;...........T.....................

                    2770       2780       2790       2800       2810       2820
                     *          *          *          *          *          *
syn1T.mze    CTGAGCGTGATCCCCGGCGTGAACGCCGCCATCTTCGAGGAGCTGGAGGGCCGCATCTTC
bssyn        ------------------------------------------------------------
synful.mod   ............................................................

                    2830       2840       2850       2860       2870       2880
                     *          *          *          *          *          *
syn1T.mze    ACCGCCTTCAGCCTGTACGACGCCCGCAACGTGATCAAGAACGGCGACTTCAACAACGGC
bssyn        ------------------------------------------------------------
synful.mod   ............................................................

                    2890       2900       2910       2920       2930       2940
                     *          *          *          *          *          *
syn1T.mze    CTGAGCTGCTGGAACGTGAAGGGCCACGTGGACGTGGAGGAGCAGAACAACCACCGCAGC
bssyn        ------------------------------------------------------------
synful.mod   ............................................................

                    2950       2960       2970       2980       2990       3000
                     *          *          *          *          *          *
syn1T.mze    GTGCTGGTGGTGCCCGAGTGGGAGGCCGAGGTGAGCCAGGAGGTGCGCGTGTGCCCCGGC
bssyn        ------------------------------------------------------------
synful.mod   ............................................................
```

D0308452 - 141204

Fig. 3F

```
                    3010      3020      3030      3040      3050      3060
                     *         *         *         *         *         *
syn1T.mze    CGCGGCTACATCCTGCGCGTGACCGCCTACAAGGAGGGCTACGGCGAGGGCTGCGTGACC
bssyn        ------------------------------------------------------------
synful.mod   ............................................................

                    3070      3080      3090      3100      3110      3120
                     *         *         *         *         *         *
syn1T.mze    ATCCACGAGATCGAGAACAACACCGACGAGCTGAAGTTCAGCAACTGCGTGGAGGAGGAG
bssyn        ------------------------------------------------------------
synful.mod   ..............................C.............................

                    3130      3140      3150      3160      3170      3180
                     *         *         *         *         *         *
syn1T.mze    GTGTACCCCAACAACACCGTGACCTGCAACGACTACACCGCCACCCAGGAGGAGTACGAG
bssyn        ------------------------------------------------------------
synful.mod   ............................................................

                    3190      3200      3210      3220      3230      3240
                     *         *         *         *         *         *
syn1T.mze    GGCACCTACACCAGCCGCAACCGCGGCTACGACGGCGCCTACGAGAGCAACAGCAGCGTG
bssyn        ------------------------------------------------------------
synful.mod   ............................................................

                    3250      3260      3270      3280      3290      3300
                     *         *         *         *         *         *
syn1T.mze    CCCGCCGACTACGCCAGCGCCTACGAGGAGAAGGCCTACACCGACGGCCGCCGCGACAAC
bssyn        ------------------------------------------------------------
synful.mod   ............................................................

                    3310      3320      3330      3340      3350      3360
                     *         *         *         *         *         *
syn1T.mze    CCCTGCGAGAGCAACCGCGGCTACGGCGACTACACCCCCCTGCCCGCCGGCTACGTGACC
bssyn        ------------------------------------------------------------
synful.mod   ............................................................

                    3370      3380      3390      3400      3410      3420
                     *         *         *         *         *         *
syn1T.mze    AAGGAGCTGGAGTACTTCCCCGAGACCGACAAGGTGTGGATCGAGATCGGCGAGACCGAG
bssyn        ------------------------------------------------------------
synful.mod   ............................................................

                    3430      3440      3450      3460
                     *         *         *         *
syn1T.mze    GGCACCTTCATCGTGGACAGCGTGGAGCTGCTGCTGATGGAGGAGTAG
bssyn        ----------------------------------------....
synful.mod   ........................................
```

Fig. 4A

```
                    10         20         30         40         50         60
                    *          *          *          *          *          *
BTHKURHD  ATGGATAACAATCCGAACATCAATGAATGCATTCCTTATAATTGTTTAAGTAACCCTGAA
PMONBT    .....C.....C..A........C..........A..C..C..C..G.......A...
bssyn     .....C.....C..C........C..G.....C..C..C..C..CC.G..C.....C..G

                    70         80         90        100        110        120
                    *          *          *          *          *          *
BTHKURHD  GTAGAAGTATTAGGTGGAGAAAGAATAGAAACTGGTTACACCCCAATCGATATTTCCTTG
PMONBT    ..T.....C.T.........C.C..T.....C.........T..C.....C..C......
bssyn     ..G..G..GC.G..C..C..GC.C..C..G..C..C........C.....C..CAG.C..

                   130        140        150        160        170        180
                    *          *          *          *          *          *
BTHKURHD  TCGCTAACGCAATTTCTTTTGAGTGAATTTGTTCCCGGTGCTGGATTTGTGTTAGGACTA
PMONBT    ..CT.G..A..G.....GC.C..C..G..C..G..A........G..C..TC.C......
bssyn     AGC..G..C..G..C..GC....C..G..C..G.....C..C..C..C...C.G..C..G

                   190        200        210        220        230        240
                    *          *          *          *          *          *
BTHKURHD  GTTGATATAATATGGGGAATTTTTGGTCCCTCTCAATGGGACGCATTTCTTGTACAAATT
PMONBT    .....C..C..C.....T..C........A..........T.....C..G..G......
bssyn     ..G..C..C..C.....C..C..C..C...AGC..G........C..C..G..G..G..C

                   250        260        270        280        290        300
                    *          *          *          *          *          *
BTHKURHD  GAACAGTTAATTAACCAAAGAATAGAAGAATTCGCTAGGAACCAAGCCATTTCTAGATTA
PMONBT    ..G.....G..C.....G..G..C.....G.....C........G.....C.....G..G
bssyn     ..G...C.G..C.....GC.C..C..G..G.....CC.C.....G.....CAGCC.CC.G

                   310        320        330        340        350        360
                    *          *          *          *          *          *
BTHKURHD  GAAGGACTAAGCAATCTTTATCAAATTTACGCAGAATCTTTTAGAGAGTGGGAAGCAGAT
PMONBT    ......T.G.........C..C.....C..T.....GAGC..C.............C...
bssyn     ..G..C..G.....C..G..C.....C.....C..GAGC..CC.C........G..C..C

                   370        380        390        400        410        420
                    *          *          *          *          *          *
BTHKURHD  CCTACTAATCCAGCATTAAGAGAAGAGATGCGTATTCAATTCAATGACATGAACAGTGCC
PMONBT    .......C.....TC.CC.C..G..A.....................C...........C...
bssyn     ..C..C..C..C..CC.GC.C..G........C..C..G.....C...........C...

                   430        440        450        460        470        480
                    *          *          *          *          *          *
BTHKURHD  CTTACAACCGCTATTCCTCTTTTTGCAGTTCAAAATTATCAAGTTCCTCTTTTATCAGTA
PMONBT    T.G..C..A.....C..AT.G..C.....C..G..C..C...........C..G..C..G
bssyn     ..G..C.....C..C..C..G..C..C..G..G..C..C..G..G..C..GC.GAGC..G

                   490        500        510        520        530        540
                    *          *          *          *          *          *
BTHKURHD  TATGTTCAAGCTGCAAATTTACATTTATCAGTTTTGAGAGATGTTTCAGTGTTTGGACAA
PMONBT    ..C.........A..T...C.T..CC.CAGC..GC.TC....C...AGC.........G...
bssyn     ..C..G..G..C..C..CC.G..CC.GAGC..GC..C.C..C..CAGC.....C..C..G

                   550        560        570        580        590        600
                    *          *          *          *          *          *
BTHKURHD  AGGTGGGGATTTGATGCCGCGACTATCAATAGTCGTTATAATGATTTAACTAGGCTTATT
PMONBT    .........C.....T..A..C.........C.....C..C..CC.T.........G...
bssyn     C.C.....C..C..C.....C..C.....C..C..C..C..C..CC.G..CC.C..G..C
```

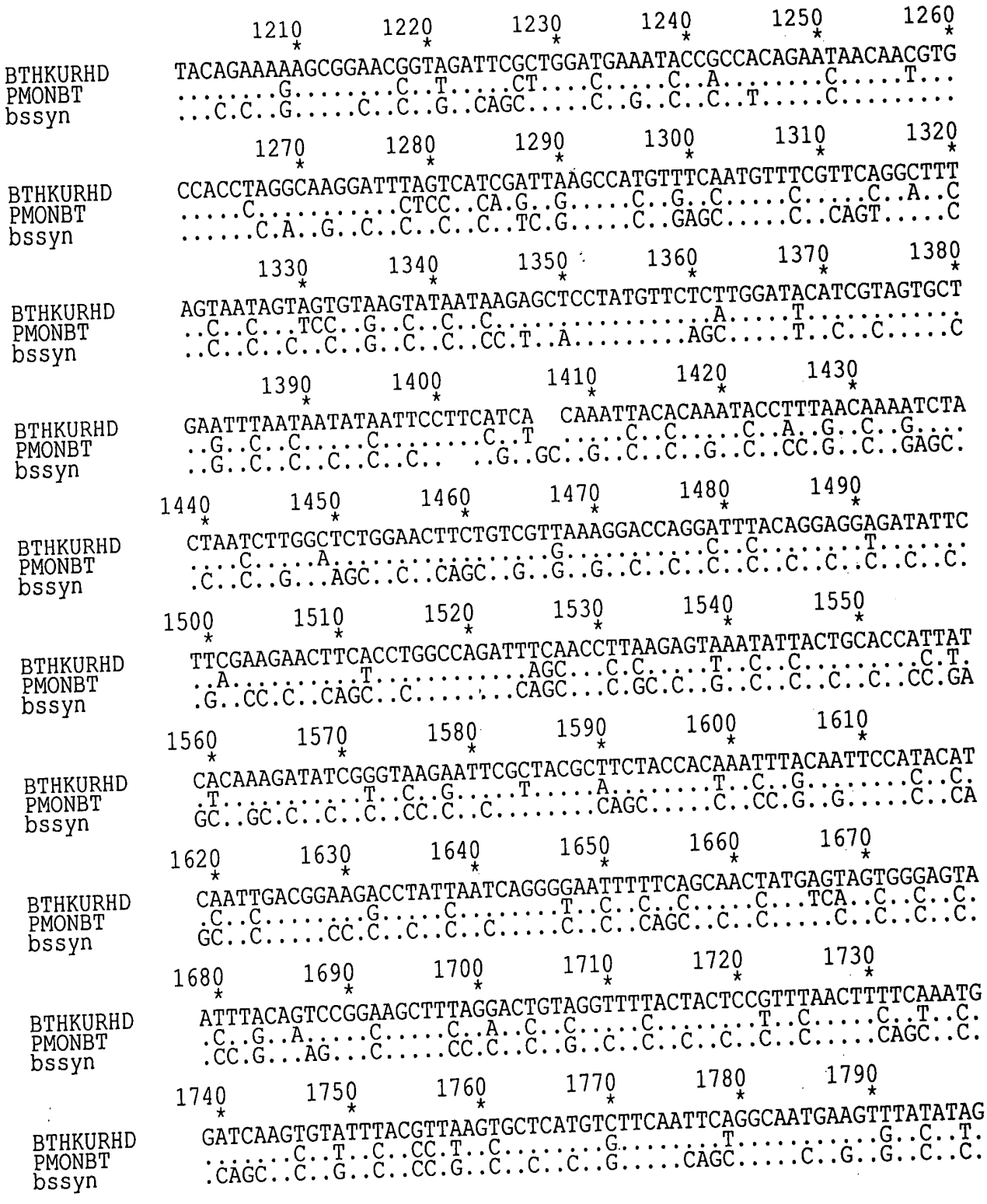
09988452-112004

Fig. 4B

```
                610        620        630        640        650        660
                *          *          *          *          *          *
BTHKURHD  GGCAACTATACAGATCATGCTGTACGCTGGTACAATACGGGATTAGAGCGTGTATGGGGA
PMONBT    ..A.....C..C..C..C.....T..T........C..T..C..G........C.....T
bssyn     ........C..C..C..C..C..G..........C..C..CC.G.....C..G.....T

                670        680        690        700        710        720
                *          *          *          *          *          *
BTHKURHD  CCGGATTCTAGAGATTGGATAAGATATAATCAATTTAGAAGAGAATTAACACTAACTGTA
PMONBT    ..T.................T.....C..C..G..C..G........G..C..C..A..T
bssyn     ..C..CAGCC.C..C.....C..G..C..C..G..CC.CC.C..GC.G..C..G..C..G

                730        740        750        760        770        780
                *          *          *          *          *          *
BTHKURHD  TTAGATATCGTTTCTCTATTTCCGAACTATGATAGTAGAACGTATCCAATTCGAACAGTT
PMONBT    ..G..C..T..G.....C..C..........CTCC.....C..C..T..C..T.....G
bssyn     C.G..C.....GAGC..G..C..C.....C..C..CC.C..C..C..C..C..C..C..G

                790        800        810        820        830        840
                *          *          *          *          *          *
BTHKURHD  TCCCAATTAACAAGAGAAATTTATACAAACCCAGTATTAGAAAATTTTGATGGTAGTTTT
PMONBT    .....C.T..C.....C.....T.....TC.T..G..C..C..C.....C..C
bssyn     AG...GC.G..CC.C..G.....C..C.....C..GC.G..G..C..C..C..C..C..C

                850        860        870        880        890        900
                *          *          *          *          *          *
BTHKURHD  CGAGGCTCGGCTCAGGGCATAGAAGGAAGTATTAGGAGTCCACATTTGATGGATATACTT
PMONBT    ..T..T..T..C..A..T..C.....CTCC..C.....C.....C........C..CT.G
bssyn     ..C...AGC..C........C..G..C..C..CC.C..C..C..CC.......C..C..G

                910        920        930        940        950        960
                *          *          *          *          *          *
BTHKURHD  AACAGTATAACCATCTATACGGATGCTCATAGAGGAGAATATTATTGGTCAGGGCATCAA
PMONBT    .....C.....T.....C.GC.........C.......G.....C.....T..A..C..G
bssyn     .....C..C.........C..C..C..C..CC.C..C..G..C..C...AGC..C..C..G

                970        980        990        1000       1010       1020
                *          *          *          *          *          *
BTHKURHD  ATAATGGCTTCTCCTGTAGGGTTTTCGGGGCCAGAATTCACTTTTCCGCTATATGGAACT
PMONBT    ..C.....C.....A..T..A..CAGC.....C..G..T..C.....T..C.........
bssyn     ..C.....CAGC..C..C..C..CAGC..C..C..G.....C..C..C..G..C..C..C

                1030       1040       1050       1060       1070       1080
                *          *          *          *          *          *
BTHKURHD  ATGGGAAATGCAGCTCCACAACAACGTATTGTTGCTCAACTAGGTCAGGGCGTGTATAGA
PMONBT    .......C..C.....................C.....................T..C..C...
bssyn     .....C..C..T..A..T..G..G..C..C..G..A..G..G..C.....A.....CC.C

                1090       1100       1110       1120       1130       1140
                *          *          *          *          *          *
BTHKURHD  ACATTATCGTCCACTTTATATAGAAGACCTTTTAATATAGGGATAAATAATCAACAACTA
PMONBT    ..C..G..T.....C..G..C.........C..C.....C..T..C..C..C..G.....T
bssyn     ..CC.GAGCAG...CC.G..CC.TC.......C..C..C..C..C..C..C..G..G..G

                1150       1160       1170       1180       1190       1200
                *          *          *          *          *          *
BTHKURHD  TCTGTTCTTGACGGGACAGAATTTGCTTATGGAACCTCCTCAAATTTGCCATCCGCTGTA
PMONBT    ..C...........A.....G..C..C.............T..T..C..............T
bssyn     AGC..G..G.....C..C..G..C..C..C..C...AG.AGC..CC....CAG...C..G
```

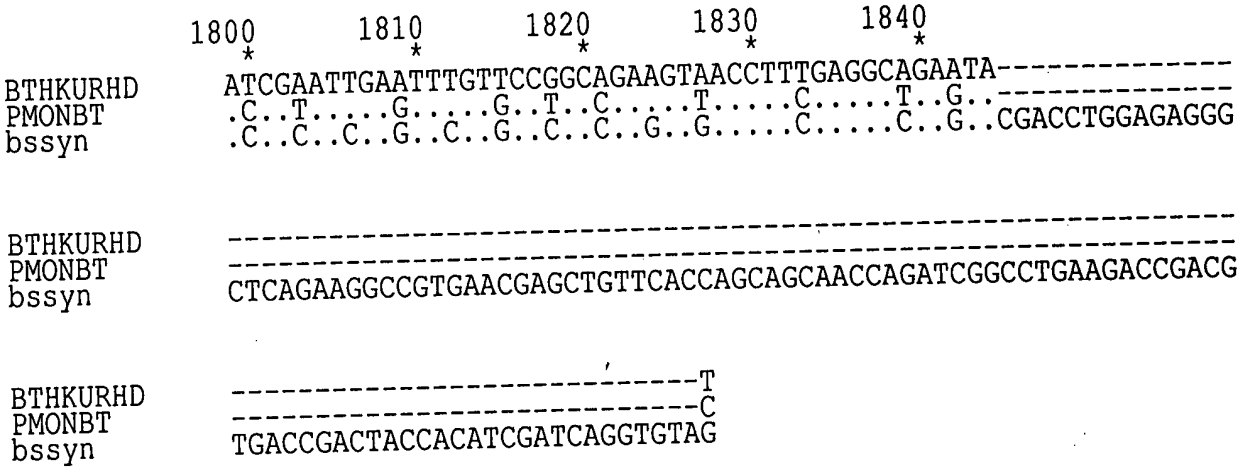
Docket: 47205-0945

Fig. 4C



10021425+9866

Fig. 4D



09934650 - 14021998

Fig. 5A

```
                    10         20         30         40         50         60
                     *          *          *          *          *          *
PMONBT   ATGGACAACAACCCAAACATCAACGAATGCATTCCATACAACTGCTTGAGTAACCCAGAA
bssyn    ............C..........G.....C..C.........C....C.....C..G

                    70         80         90        100        110        120
                     *          *          *          *          *          *
PMONBT   GTTGAAGTACTTGGTGGAGAACGCATTGAAACCGGTTACACTCCCATCGACATCTCCTTG
bssyn    ..G..G..G..G..C..C..G.....C..G.....C.....C...........AG.C..

                   130        140        150        160        170        180
                     *          *          *          *          *          *
PMONBT   TCCTTGACACAGTTTCTGCTCAGCGAGTTCGTGCCAGGTGCTGGGTTCGTTCTCGGACTA
bssyn    AG.C....C.....C.....G.............C..C..C..C.....G..G..C..G

                   190        200        210        220        230        240
                     *          *          *          *          *          *
PMONBT   GTTGACATCATCTGGGGTATCTTTGGTCCATCTCAATGGGATGCATTCCTGGTGCAAATT
bssyn    ..G............C.....C..C..CAGC..G.....C..C...........G..C

                   250        260        270        280        290        300
                     *          *          *          *          *          *
PMONBT   GAGCAGTTGATCAACCAGAGGATCGAAGAGTTCGCCAGGAACCAGGCCATCTCTAGGTTG
bssyn    ......C...........C.C.....G.........C.C............AGCC.CC..

                   310        320        330        340        350        360
                     *          *          *          *          *          *
PMONBT   GAAGGATTGAGCAATCTCTACCAAATCTATGCAGAGAGCTTCAGAGAGTGGGAAGCCGAT
bssyn    ..G..CC.......C..G...........C..C.........C.C.........G.....C

                   370        380        390        400        410        420
                     *          *          *          *          *          *
PMONBT   CCTACTAACCCAGCTCTCCGCGAGGAAATGCGTATTCAATTCAACGACATGAACAGCGCC
bssyn    ..C..C.....C..C..G........G.....C..C..G....................

                   430        440        450        460        470        480
                     *          *          *          *          *          *
PMONBT   TTGACCACAGCTATCCCATTGTTCGCAGTCCAGAACTACCAAGTTCCTCTCTTGTCCGTG
bssyn    C.......C..C.....CC.......C..G...........G..G..C..GC..AG....

                   490        500        510        520        530        540
                     *          *          *          *          *          *
PMONBT   TACGTTCAAGCAGCTAATCTTCACCTCAGCGTGCTTCGAGACGTTAGCGTGTTTGGGCAA
bssyn    .....G..G..C..C..C..G.....G........G..C.....C........C..C..G

                   550        560        570        580        590        600
                     *          *          *          *          *          *
PMONBT   AGGTGGGGATTCGATGCTGCAACCATCAATAGCCGTTACAACGACCTTACTAGGCTGATT
bssyn    C.C.....C.....C..C..C........C.....C...........G..CC.C.....C

                   610        620        630        640        650        660
                     *          *          *          *          *          *
PMONBT   GGAAACTACACCGACCACGCTGTTCGTTGGTACAACACTGGCTTGGAGCGTGTCTGGGGT
bssyn    ..C................C..G..C...........C...C.......C..G......

                   670        680        690        700        710        720
                     *          *          *          *          *          *
PMONBT   CCTGATTCTAGAGATTGGATTAGATACAACCAGTTCAGGAGAGAATTGACCCTCACAGTT
bssyn    ..C..CAGCC.C..C.....C..G...........C.CC.C..GC.......G..C..G
```

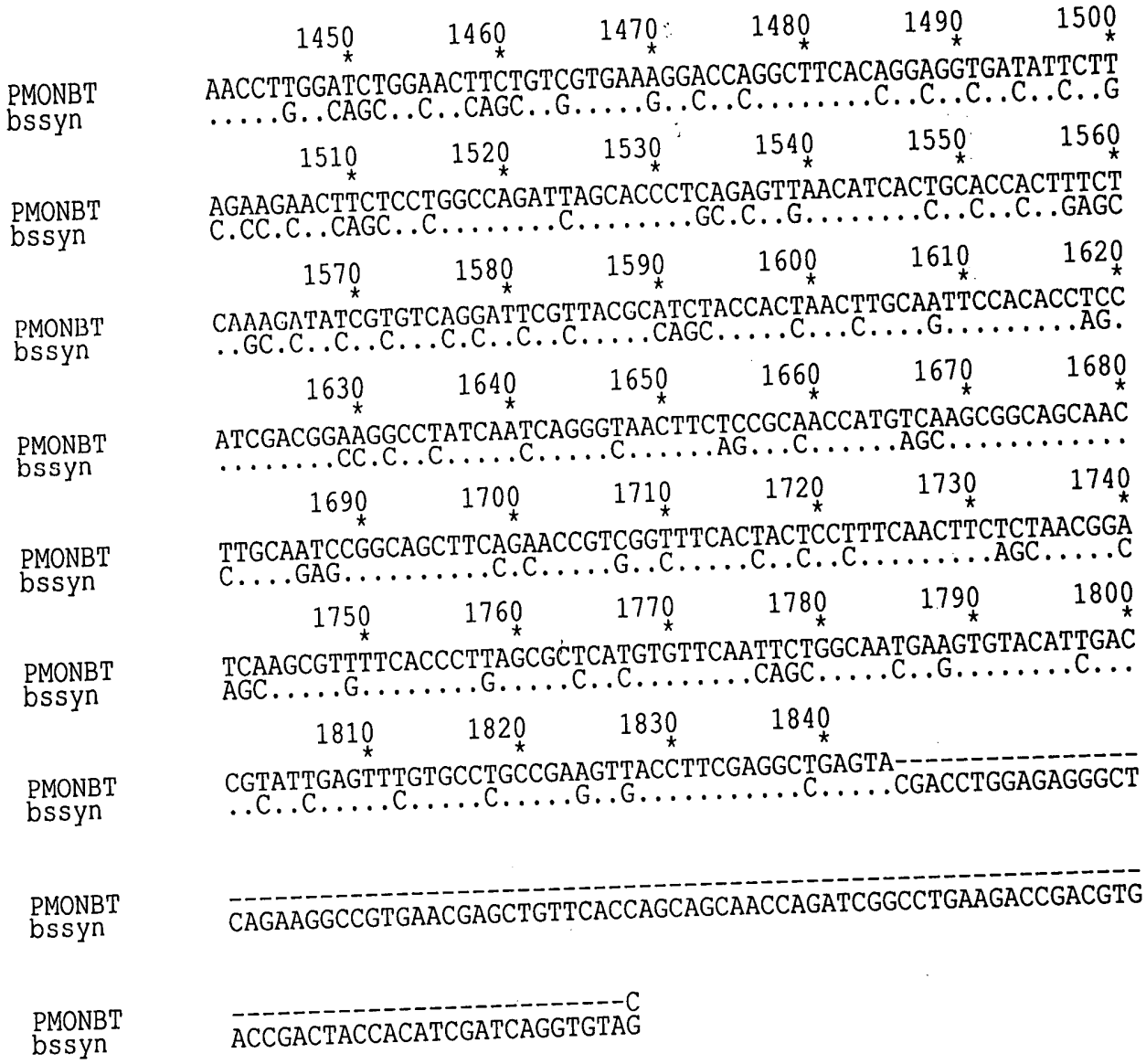
Docket No. 4598-4205

Fig. 5B

```
                730       740       750       760       770       780
                *         *         *         *         *         *
PMONBT          TTGGACATTGTGTCTCTCTTCCCGAACTATGACTCCAGAACCTACCCTATCCGTACAGTG
bssyn           C.......C...AGC..G.....C.....C...AG.C.C........C.....C..C...

                790       800       810       820       830       840
                *         *         *         *         *         *
PMONBT          TCCCAACTTACCAGAGAAATCTATACTAACCCAGTTCTTGAGAACTTCGACGGTAGCTTC
bssyn           AG...G..G...C.C..G..T..C..C.....C..G..G.............C......

                850       860       870       880       890       900
                *         *         *         *         *         *
PMONBT          CGTGGTTCTGCCCAAGGTATCGAAGGCTCCATCAGGAGCCCACACTTGATGGACATCTTG
bssyn           ..C..CAGC.....G..C.....G...AG....C.C.....C...C...........C..

                910       920       930       940       950       960
                *         *         *         *         *         *
PMONBT          AACAGCATAACTATCTACAGCGATGCTCACAGAGGAGAGTATTACTGGTCTGGACACCAG
bssyn           ........C..C........C...C..C...C.C..C.....C......AGC..C......

                970       980       990       1000      1010      1020
                *         *         *         *         *         *
PMONBT          ATCATGGCCTCTCCAGTTGGATTCAGCGGGCCCGAGTTTACCTTTCCTCTCTATGGAACT
bssyn           .........AGC..C..C..C.........C.........C.....C..C..G..C..C..C

                1030      1040      1050      1060      1070      1080
                *         *         *         *         *         *
PMONBT          ATGGGAAACGCCGCTCCACAACAACGTATCGTTGCTCAACTAGGTCAGGGTGTCTACAGA
bssyn           .....C.....T..A..T..G..G..C.....G..A..G..G..C.....A..G...C.C

                1090      1100      1110      1120      1130      1140
                *         *         *         *         *         *
PMONBT          ACCTTGTCTTCCACCTTGTACAGAAGACCCTTCAATATCGGTATCAACAACCAGCAACTT
bssyn           ...C..AGCAG....C.....C.TC....T.....C.....C..............G..G

                1150      1160      1170      1180      1190      1200
                *         *         *         *         *         *
PMONBT          TCCGTTCTTGACGGAACAGAGTTCGCCTATGGAACCTCTTCTAACTTGCCATCCGCTGTT
bssyn           AG...G..G.....C..C...........C..C...AGCAGC...C....CAG...C..G

                1210      1220      1230      1240      1250      1260
                *         *         *         *         *         *
PMONBT          TACAGAAAGAGCGGAACCGTTGATTCCTTGGACGAAATCCCACCACAGAACAACAATGTG
bssyn           ...C.C........C.....G..CAG.C.......G.....C..T...........C...

                1270      1280      1290      1300      1310      1320
                *         *         *         *         *         *
PMONBT          CCACCCAGGCAAGGATTCTCCCACAGGTTGAGCCACGTGTCCATGTTCCGTTCCGGATTC
bssyn           .....TC.A..G..C...AG....C.TC...........AG.........CAGT..C...

                1330      1340      1350      1360      1370      1380
                *         *         *         *         *         *
PMONBT          AGCAACAGTTCCGTGAGCATCATCAGAGCTCCTATGTTCTCATGGATTCATCGTAGTGCT
bssyn           ........CAG.............C.T..A.........AGC.........C..C.....C

                1390      1400      1410      1420      1430      1440
                *         *         *         *         *         *
PMONBT          GAGTTCAACAATATCATTCCTTCCTCTCAAATCACCCAAATCCCATTGACCAAGTCTACT
bssyn           ..........C.....C..CAG.AGC..G........G.....CC.........AGC..C
```

D9884552 - 112004

Fig. 5C



09668452.1420

Fig. 6A

```
64   ATGGACCTGC TGCCCGACGC CCGCATCGAG GACAGCCTGT GCATCGCCGA GGGCAACAAC
     MetAspLeu LeuProAsp AlaArgIleGlu AspSerLeu CysIleAla GluGlyAsnAsn

124  ATCGACCCCT TCGTGAGCGC CAGCACCGTG CAGACCGGCA TCAACATCGC CGGCCGCATC
     IleAspPro PheValSer AlaSerThrVal GlnThrGly IleAsnIle AlaGlyArgIle

184  CTGGGCGTGC TGGGCGTGCC CTTCGCCGGC CAGCTGGCCA GCTTCTACAG CTTCCTGGTG
     LeuGlyVal LeuGlyVal ProPheAlaGly GlnLeuAla SerPheTyr SerPheLeuVal

244  GGCGAGCTGT GGCCCCGCGG CCGCGACCAG TGGGAGATCT TCCTGGAGCA CGTGGAGCAG
     GlyGluLeu TrpProArg GlyArgAspGln TrpGluIle PheLeuGlu HisValGluGln

304  CTGATCAACC AGCAGATCAC CGAGAACGCC CGCAACACCG CCCTGGCCCG CCTGCAGGGC
     LeuIleAsn GlnGlnIle ThrGluAsnAla ArgAsnThr AlaLeuAla ArgLeuGlnGly

364  CTGGGCGACA GCTTCCGCGC CTACCAGCAG AGCCTGGAGG ACTGGCTGGA GAACCGCGAC
     LeuGlyAsp SerPheArg AlaTyrGlnGln SerLeuGlu AspTrpLeu GluAsnArgAsp

424  GACGCCCGCA CCCGCAGCGT GCTGTACACC CAGTACATCG CCCTGGAGCT GGACTTCCTG
     AspAlaArg ThrArgSer ValLeuTyrThr GlnTyrIle AlaLeuGlu LeuAspPheLeu

484  AACGCCATGC CCCTGTTCGC CATCCGCAAC CAGGAGGTGC CCCTGCTGAT GGTGTACGCC
     AsnAlaMet ProLeuPhe AlaIleArgAsn GlnGluVal ProLeuLeu MetValTyrAla

544  CAGGCCGCCA ACCTGCACCT GCTGCTGCTG CGCGACGCCA GCCTGTTCGG CAGCGAGTTC
     GlnAlaAla AsnLeuHis LeuLeuLeuLeu ArgAspAla SerLeuPhe GlySerGluPhe

604  GGCCTGACCA GCCAGGAGAT CCAGCGCTAC TACGAGCGCC AGGTGGAGCG CACCCGCGAC
     GlyLeuThr SerGlnGlu IleGlnArgTyr TyrGluArg GlnValGlu ArgThrArgAsp

664  TACAGCGACT ACTGCGTGGA GTGGTACAAC ACCGGCCTGA ACAGCCTGCG CGGCACCAAC
     TyrSerAsp TyrCysVal GluTrpTyrAsn ThrGlyLeu AsnSerLeu ArgGlyThrAsn

724  GCCGCCAGCT GGGTGCGCTA CAACCAGTTC CGCCGCGACC TGACCCTGGG CGTGCTGGAC
     AlaAlaSer TrpValArg TyrAsnGlnPhe ArgArgAsp LeuThrLeu GlyValLeuAsp

784  CTGGTGGCCC TGTTCCCCAG CTACGACACC CGCACCTACC CCATCAACAC CAGCGCCCAG
     LeuValAla LeuPhePro SerTyrAspThr ArgThrTyr ProIleAsn ThrSerAlaGln

844  CTGACCCGCG AGGTGTACAC CGACGCCATC GGCGCCACCG GCGTGAACAT GGCCAGCATG
     LeuThrArg GluValTyr ThrAspAlaIle GlyAlaThr GlyValAsn MetAlaSerMet

904  AACTGGTACA ACAACAACGC CCCCAGCTTC AGCGCCATCG AGGCCGCCGC CATCCGCAGC
     AsnTrpTyr AsnAsnAsn AlaProSerPhe SerAlaIle GluAlaAla AlaIleArgSer

964  CCCCACCTGC TGGACTTCCT GGAGCAGCTG ACCATCTTCA GCGCCAGCAG CCGCTGGAGC
     ProHisLeu LeuAspPhe LeuGluGlnLeu ThrIlePhe SerAlaSer SerArgTrpSer

1024 AACACCCGCC ACATGACCTA CTGGCGCGGC CACACCATCC AGAGCCGCCC CATCGGCGGC
     AsnThrArg HisMetThr TyrTrpArgGly HisThrIle GlnSerArg ProIleGlyGly
```

5,968,457 - 19 Oct 1999

Fig. 6B

```
1084  GGCCTGAACA CCAGCACCCA CGGCGCCACC AACACCAGCA TCAACCCCGT GACCCTGCGC
      GlyLeuAsn ThrSerThr HisGlyAlaThr AsnThrSer IleAsnPro ValThrLeuArg

1144  TTCGCCAGCC GCGACGTGTA CCGCACCGAG AGCTACGCCG GCGTGCTGCT GTGGGGCATC
      PheAlaSer ArgAspVal TyrArgThrGlu SerTyrAla GlyValLeu LeuTrpGlyIle

1204  TACCTGGAGC CCATCCACGG CGTGCCCACC GTGCGCTTCA ACTTCACCAA CCCCCAGAAC
      TyrLeuGlu ProIleHis GlyValProThr ValArgPhe AsnPheThr AsnProGlnAsn

1264  ATCAGCGACC GCGGCACCGC CAACTACAGC CAGCCCTACG AGAGCCCCGG CCTGCAGCTG
      IleSerAsp ArgGlyThr AlaAsnTyrSer GlnProTyr GluSerPro GlyLeuGlnLeu

1324  AAGGACAGCG AGACCGAGCT GCCCCCCGAG ACCACCGAGC GCCCCAACTA CGAGAGCTAC
      LysAspSer GluThrGlu LeuProProGlu ThrThrGlu ArgProAsn TyrGluSerTyr

1384  AGCCACCGCC TGAGCCACAT CGGCATCATC CTGCAGAGCC GCGTGAACGT GCCCGTGTAC
      SerHisArg LeuSerHis IleGlyIleIle LeuGlnSer ArgValAsn ValProValTyr

1444  AGCTGGACCC ACCGCAGCGC CGACCGCACC AACACCATCG GCCCCAACCG CATCACCCAG
      SerTrpThr HisArgSer AlaAspArgThr AsnThrIle GlyProAsn ArgIleThrGln

1504  ATCCCCATGG TGAAGGCCAG CGAGCTGCCC CAGGGCACCA CCGTGGTGCG CGGCCCCGGC
      IleProMet ValLysAla SerGluLeuPro GlnGlyThr ThrValVal ArgGlyProGly

1564  TTCACCGGCG GCGACATCCT GCGCCGCACC AACACCGGCG GCTTCGGCCC CATCCGCGTG
      PheThrGly GlyAspIle LeuArgArgThr AsnThrGly GlyPheGly ProIleArgVal

1624  ACCGTGAACG GCCCCCTGAC CCAGCGCTAC CGCATCGGCT TCCGCTACGC CAGCACCGTG
      ThrValAsn GlyProLeu ThrGlnArgTyr ArgIleGly PheArgTyr AlaSerThrVal

1684  GACTTCGACT TCTTCGTGAG CCGCGGCGGC ACCACCGTGA ACAACTTCCG CTTCCTGCGC
      AspPheAsp PhePheVal SerArgGlyGly ThrThrVal AsnAsnPhe ArgPheLeuArg

1744  ACCATGAACA GCGGCGACGA GCTGAAGTAC GGCAACTTCG TGCGCCGCGC CTTCACCACC
      ThrMetAsn SerGlyAsp GluLeuLysTyr GlyAsnPhe ValArgArg AlaPheThrThr

1804  CCCTTCACCT TCACCCAGAT CCAGGACATC ATCCGCACCA GCATCCAGGG CCTGAGCGGC
      ProPheThr PheThrGln IleGlnAspIle IleArgThr SerIleGln GlyLeuSerGly

1864  AACGGCGAGG TGTACATCGA CAAGATCGAG ATCATCCCCG TGACCGCCAC CTTCGAGGCC
      AsnGlyGlu ValTyrIle AspLysIleGlu IleIlePro ValThrAla ThrPheGluAla

1924  GAGTACGACC TGGAGCGCGC CCAGGAGGCC GTGAACGCCC TGTTCACCAA CACCAACCCC
      GluTyrAsp LeuGluArg AlaGlnGluAla ValAsnAla LeuPheThr AsnThrAsnPro

1984  CGCCGCCTGA AGACCGACGT GACCGACTAC CACATCGACC AGGTGAGCAA CCTGGTGGCC
      ArgArgLeu LysThrAsp ValThrAspTyr HisIleAsp GlnValSer AsnLeuValAla

2044  TGCCTGAGCG ACGAGTTCTG CCTGGACGAG AAGCGCGAGC TGCTGGAGAA GGTGAAGTAC
      CysLeuSer AspGluPhe CysLeuAspGlu LysArgGlu LeuLeuGlu LysValLysTyr
```

Proof - 5,986,452

Fig. 6C

```
2104  GCCAAGCGCC TGAGCGACGA GCGCAACCTG CTGCAGGACC CCAACTTCAC CAGCATCAAC
      AlaLysArg LeuSerAsp GluArgAsnLeu LeuGlnAsp ProAsnPhe ThrSerIleAsn

2164  AAGCAGCCCG ACTTCATCAG CACCAACGAG CAGAGCAACT TCACCAGCAT CCACGAGCAG
      LysGlnPro AspPheIle SerThrAsnGlu GlnSerAsn PheThrSer IleHisGluGln

2224  AGCGAGCACG GCTGGTGGGG CAGCGAGAAC ATCACCATCC AGGAGGGCAA CGACGTGTTC
      SerGluHis GlyTrpTrp GlySerGluAsn IleThrIle GlnGluGly AsnAspValPhe

2284  AAGGAGAACT ACGTGACCCT GCCCGGCACC TTCAACGAGT GCTACCCCAC CTACCTGTAC
      LysGluAsn TyrValThr LeuProGlyThr PheAsnGlu CysTyrPro ThrTyrLeuTyr

2344  CAGAAGATCG GCGAGAGCGA GCTGAAGGCC TACACCCGCT ACCAGCTGCG CGGCTACATC
      GlnLysIle GlyGluSer GluLeuLysAla TyrThrArg TyrGlnLeu ArgGlyTyrIle

2404  GAGGACAGCC AGGACCTGGA GATCTACCTG ATCCGCTACA ACGCCAAGCA CGAGACCCTG
      GluAspSer GlnAspLeu GluIleTyrLeu IleArgTyr AsnAlaLys HisGluThrLeu

2464  GACGTGCCCG GCACCGAGAG CCTGTGGCCC CTGAGCGTGG AGAGCCCCAT CGGCCGCTGC
      AspValPro GlyThrGlu SerLeuTrpPro LeuSerVal GluSerPro IleGlyArgCys

2524  GGCGAGCCCA ACCGCTGCGC CCCCCACTTC GAGTGGAACC CCGACCTGGA CTGCAGCTGC
      GlyGluPro AsnArgCys AlaProHisPhe GluTrpAsn ProAspLeu AspCysSerCys

2584  CGCGACGGCG AGAAGTGCGC CCACCACAGC CACCACTTCA GCCTGGACAT CGACGTGGGC
      ArgAspGly GluLysCys AlaHisHisSer HisHisPhe SerLeuAsp IleAspValGly

2644  TGCACCGACC TGCACGAGAA CCTGGGCGTG TGGGTGGTGT TCAAGATCAA GACCCAGGAG
      CysThrAsp LeuHisGlu AsnLeuGlyVal TrpValVal PheLysIle LysThrGlnGlu

2704  GGCCACGCCC GCCTGGGCAA CCTGGAGTTC ATCGAGGAGA AGCCCCTGCT GGGCGAGGCC
      GlyHisAla ArgLeuGly AsnLeuGluPhe IleGluGlu LysProLeu LeuGlyGluAla

2764  CTGAGCCGCG TGAAGCGCGC CGAGAAGAAG TGGCGCGACA AGCGCGAGAA GCTGCAGCTG
      LeuSerArg ValLysArg AlaGluLysLys TrpArgAsp LysArgGlu LysLeuGlnLeu

2824  GAGACCAAGC GCGTGTACAC CGAGGCCAAG GAGGCCGTGG ACGCCCTGTT CGTGGACAGC
      GluThrLys ArgValTyr ThrGluAlaLys GluAlaVal AspAlaLeu PheValAspSer

2884  CAGTACGACC GCCTGCAGGC CGACACCAAC ATCGGCATGA TCCACGCCGC CGACAAGCTG
      GlnTyrAsp ArgLeuGln AlaAspThrAsn IleGlyMet IleHisAla AlaAspLysLeu

2944  GTGCACCGCA TCCGCGAGGC CTACCTGAGC GAGCTGCCCG TGATCCCCGG CGTGAACGCC
      ValHisArg IleArgGlu AlaTyrLeuSer GluLeuPro ValIlePro GlyValAsnAla

3004  GAGATCTTCG AGGAGCTGGA GGGCCACATC ATCACCGCCA TCAGCCTGTA CGACGCCCGC
      GluIlePhe GluGluLeu GluGlyHisIle IleThrAla IleSerLeu TyrAspAlaArg
```

EP 0 984 042 A2 - 15 03 2000

Fig. 6D

```
3064  AACGTGGTGA AGAACGGCGA CTTCAACAAC GGCCTGACCT GCTGGAACGT GAAGGGCCAC
      AsnValVal LysAsnGly AspPheAsnAsn GlyLeuThr CysTrpAsn ValLysGlyHis

3124  GTGGACGTGC AGCAGAGCCA CCACCGCAGC GACCTGGTGA TCCCCGAGTG GGAGGCCGAG
      ValAspVal GlnGlnSer HisHisArgSer AspLeuVal IleProGlu TrpGluAlaGlu

3184  GTGAGCCAGG CCGTGCGCGT GTGCCCCGGC TGCGGCTACA TCCTGCGCGT GACCGCCTAC
      ValSerGln AlaValArg ValCysProGly CysGlyTyr IleLeuArg ValThrAlaTyr

3244  AAGGAGGGCT ACGGCGAGGG CTGCGTGACC ATCCACGAGA TCGAGAACAA CACCGACGAG
      LysGluGly TyrGlyGlu GlyCysValThr IleHisGlu IleGluAsn AsnThrAspGlu

3304  CTGAAGTTCA AGAACCGCGA GGAGGAGGAG GTGTACCCCA CCGACACCGG CACCTGCAAC
      LeuLysPhe LysAsnArg GluGluGluGlu ValTyrPro ThrAspThr GlyThrCysAsn

3364  GACTACACCG CCCACCAGGG CACCGCCGGC TGCGCCGACG CCTGCAACAG CCGCAACGCC
      AspTyrThr AlaHisGln GlyThrAlaGly CysAlaAsp AlaCysAsn SerArgAsnAla

3424  GGCTACGAGG ACGCCTACGA GGTGGACACC ACCGCCAGCG TGAACTACAA GCCCACCTAC
      GlyTyrGlu AspAlaTyr GluValAspThr ThrAlaSer ValAsnTyr LysProThrTyr

3484  GAGGAGGAGA CCTACACCGA CGTGCGCCGC GACAACCACT GCGAGTACGA CCGCGGCTAC
      GluGluGlu ThrTyrThr AspValArgArg AspAsnHis CysGluTyr AspArgGlyTyr

3544  GTGAACTACC CCCCCGTGCC CGCCGGCTAC GTGACCAAGG AGCTGGAGTA CTTCCCCGAG
      ValAsnTyr ProProVal ProAlaGlyTyr ValThrLys GluLeuGlu TyrPheProGlu

3604  ACCGACACCG TGTGGATCGA GATCGGCGAG ACCGAGGGCA AGTTCATCGT GGACAGCGTG
      ThrAspThr ValTrpIle GluIleGlyGlu ThrGluGly LysPheIle ValAspSerVal

3664  GAGCTGCTGC TGATGGAGGA GTAG
      GluLeuLeu LeuMetGlu Glu---
```

Top-Secret-2504680

Fig. 7A

SEQUENCE OF THE FULL-LENGTH HYBRID SYNTHETIC/NATIVE CRYIA(B) CHIMERIC GENE
The fusion point between the synthetic and native coding sequences is indicated by a slash (/) in the sequence.

```
   1  ATGGACAACA ACCCCAACAT CAACGAGTGC ATCCCCTACA ACTGCCTGAG CAACCCCGAG
      MetAspAsn AsnProAsn IleAsnGluCys IleProTyr AsnCysLeu SerAsnProGlu

  61  GTGGAGGTGC TGGGCGGCGA GCGCATCGAG ACCGGCTACA CCCCCATCGA CATCAGCCTG
      ValGluVal LeuGlyGly GluArgIleGlu ThrGlyTyr ThrProIle AspIleSerLeu

 121  AGCCTGACCC AGTTCCTGCT GAGCGAGTTC GTGCCCGGCG CCGGCTTCGT GCTGGGCCTG
      SerLeuThr GlnPheLeu LeuSerGluPhe ValProGly AlaGlyPhe ValLeuGlyLeu

 181  GTGGACATCA TCTGGGGCAT CTTCGGCCCC AGCCAGTGGG ACGCCTTCCT GGTGCAGATC
      ValAspIle IleTrpGly IlePheGlyPro SerGlnTrp AspAlaPhe LeuValGlnIle

 241  GAGCAGCTGA TCAACCAGCG CATCGAGGAG TTCGCCCGCA ACCAGGCCAT CAGCCGCCTG
      GluGlnLeu IleAsnGln ArgIleGluGlu PheAlaArg AsnGlnAla IleSerArgLeu

 301  GAGGGCCTGA GCAACCTGTA CCAAATCTAC GCCGAGAGCT TCCGCGAGTG GGAGGCCGAC
      GluGlyLeu SerAsnLeu TyrGlnIleTyr AlaGluSer PheArgGlu TrpGluAlaAsp

 361  CCCACCAACC CCGCCCTGCG CGAGGAGATG CGCATCCAGT TCAACGACAT GAACAGCGCC
      ProThrAsn ProAlaLeu ArgGluGluMet ArgIleGln PheAsnAsp MetAsnSerAla

 421  CTGACCACCG CCATCCCCCT GTTCGCCGTG CAGAACTACC AGGTGCCCCT GCTGAGCGTG
      LeuThrThr AlaIlePro LeuPheAlaVal GlnAsnTyr GlnValPro LeuLeuSerVal

 481  TACGTGCAGG CCGCCAACCT GCACCTGAGC GTGCTGCGCG ACGTCAGCGT GTTCGGCCAG
      TyrValGln AlaAlaAsn LeuHisLeuSer ValLeuArg AspValSer ValPheGlyGln

 541  CGCTGGGGCT TCGACGCCGC CACCATCAAC AGCCGCTACA ACGACCTGAC CCGCCTGATC
      ArgTrpGly PheAspAla AlaThrIleAsn SerArgTyr AsnAspLeu ThrArgLeuIle

 601  GGCAACTACA CCGACCACGC CGTGCGCTGG TACAACACCG GCCTGGAGCG CGTGTGGGGT
      GlyAsnTyr ThrAspHis AlaValArgTrp TyrAsnThr GlyLeuGlu ArgValTrpGly

 661  CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTG
      ProAspSer ArgAspTrp IleArgTyrAsn GlnPheArg ArgGluLeu ThrLeuThrVal

 721  CTGGACATCG TGAGCCTGTT CCCCAACTAC GACAGCCGCA CCTACCCCAT CCGCACCGTG
      LeuAspIle ValSerLeu PheProAsnTyr AspSerArg ThrTyrPro IleArgThrVal

 781  AGCCAGCTGA CCCGCGAGAT TTACACCAAC CCCGTGCTGG AGAACTTCGA CGGCAGCTTC
      SerGlnLeu ThrArgGlu IleTyrThrAsn ProValLeu GluAsnPhe AspGlySerPhe

 841  CGCGGCAGCG CCCAGGGCAT CGAGGGCAGC ATCCGCAGCC CCCACCTGAT GGACATCCTG
      ArgGlySer AlaGlnGly IleGluGlySer IleArgSer ProHisLeu MetAspIleLeu

 901  AACAGCATCA CCATCTACAC CGACGCCCAC CGCGGCGAGT ACTACTGGAG CGGCCACCAG
      AsnSerIle ThrIleTyr ThrAspAlaHis ArgGlyGlu TyrTyrTrp SerGlyHisGln
```

PCT/US98/14774

Fig. 7B

```
961  ATCATGGCCA GCCCCGTCGG CTTCAGCGGC CCCGAGTTCA CCTTCCCCCT GTACGGCACC
     IleMetAla SerProVal GlyPheSerGly ProGluPhe ThrPhePro LeuTyrGlyThr

1021 ATGGGCAACG CTGCACCTCA GCAGCGCATC GTGGCACAGC TGGGCCAGGG AGTGTACCGC
     MetGlyAsn AlaAlaPro GlnGlnArgIle ValAlaGln LeuGlyGln GlyValTyrArg

1081 ACCCTGAGCA GCACCCTGTA CCGTCGACCT TTCAACATCG GCATCAACAA CCAGCAGCTG
     ThrLeuSer SerThrLeu TyrArgArgPro PheAsnIle GlyIleAsn AsnGlnGlnLeu

1141 AGCGTGCTGG ACGGCACCGA GTTCGCCTAC GGCACCAGCA GCAACCTGCC CAGCGCCGTG
     SerValLeu AspGlyThr GluPheAlaTyr GlyThrSer SerAsnLeu ProSerAlaVal

1201 TACCGCAAGA GCGGCACCGT GGACAGCCTG GACGAGATCC CCCCTCAGAA CAACAACGTG
     TyrArgLys SerGlyThr ValAspSerLeu AspGluIle ProProGln AsnAsnAsnVal

1261 CCACCTCGAC AGGGCTTCAG CCACCGTCTG AGCCACGTGA GCATGTTCCG CAGTGGCTTC
     ProProArg GlnGlyPhe SerHisArgLeu SerHisVal SerMetPhe ArgSerGlyPhe

1321 AGCAACAGCA GCGTGAGCAT CATCCGTGCA CCTATGTTCA GCTGGATTCA CCGCAGTGCC
     SerAsnSer SerValSer IleIleArgAla ProMetPhe SerTrpIle HisArgSerAla

1381 GAGTTCAACA ACATCATCCC CAGCAGCCAG ATCACCCAGA TCCCCCTGAC CAAGAGCACC
     GluPheAsn AsnIleIle ProSerSerGln IleThrGln IleProLeu ThrLysSerThr

1441 AACCTGGGCA GCGGCACCAG CGTGGTGAAG GGCCCCGGCT TCACCGGCGG CGACATCCTG
     AsnLeuGly SerGlyThr SerValValLys GlyProGly PheThrGly GlyAspIleLeu

1501 CGCCGCACCA GCCCCGGCCA GATCAGCACC CTGCGCGTGA ACATCACCGC CCCCCTGAGC
     ArgArgThr SerProGly GlnIleSerThr LeuArgVal AsnIleThr AlaProLeuSer

1561 CAGCGCTACC GCGTCCGCAT CCGCTACGCC AGCACCACCA ACCTGCAGTT CCACACCAGC
     GlnArgTyr ArgValArg IleArgTyrAla SerThrThr AsnLeuGln PheHisThrSer

1621 ATCGACGGCC GCCCCATCAA CCAGGGCAAC TTCAGCGCCA CCATGAGCAG CGGCAGCAAC
     IleAspGly ArgProIle AsnGlnGlyAsn PheSerAla ThrMetSer SerGlySerAsn

1681 CTGCAGAGCG GCAGCTTCCG CACCGTGGGC TTCACCACCC CCTTCAACTT CAGCAACGGC
     LeuGlnSer GlySerPhe ArgThrValGly PheThrThr ProPheAsn PheSerAsnGly

1741 AGCAGCGTGT TCACCCTGAG CGCCCACGTG TTCAACAGCG GCAACGAGGT GTACATCGAC
     SerSerVal PheThrLeu SerAlaHisVal PheAsnSer GlyAsnGlu ValTyrIleAsp

1801 CGCATCGAGT TCGTGCCCGC CGAGGTGACC TTCGAGGCCG AGTACGACCT GGAGAGGGCT
     ArgIleGlu PheValPro AlaGluValThr PheGluAla GluTyrAsp LeuGluArgAla

1861 CAGAAGGCCG TGAACGAGCT GTTCACCAGC AGCAACCAGA TCGGCCTGAA GACCGACGTG
     GlnLysAla ValAsnGlu LeuPheThrSer SerAsnGln IleGlyLeu LysThrAspVal
```

Patent - 5,986,069

Fig. 7C

```
1921  ACCGACTACC ACATCGAT/CA AGTATCCAAT TTAGTTGAGT GTTTATCTGATGAATTTTGT
      ThrAspTyr HisIleAsp/GlnValSerAsn LeuValGlu CysLeuSer AspGluPheCys

1981  CTGGATGAAA AAAAAGAATT GTCCGAGAAA GTCAAACATG CGAAGCGACT TAGTGATGAG
      LeuAspGlu LysLysGlu LeuSerGluLys ValLysHis AlaLysArg LeuSerAspGlu

2041  CGGAATTTAC TTCAAGATCC AAACTTTAGA GGGATCAATA GACAACTAGA CCGTGGCTGG
      ArgAsnLeu LeuGlnAsp ProAsnPheArg GlyIleAsn ArgGlnLeu AspArgGlyTrp

2101  AGAGGAAGTA CGGATATTAC CATCCAAGGA GGCGATGACG TATTCAAAGA GAATTACGTT
      ArgGlySer ThrAspIle ThrIleGlnGly GlyAspAsp ValPheLys GluAsnTyrVal

2161  ACGCTATTGG GTACCTTTGA TGAGTGCTAT CCAACGTATT TATATCAAAA AATAGATGAG
      ThrLeuLeu GlyThrPhe AspGluCysTyr ProThrTyr LeuTyrGln LysIleAspGlu

2221  TCGAAATTAA AAGCCTATAC CCGTTACCAA TTAAGAGGGT ATATCGAAGA TAGTCAAGAC
      SerLysLeu LysAlaTyr ThrArgTyrGln LeuArgGly TyrIleGlu AspSerGlnAsp

2281  TTAGAAATCT ATTTAATTCG CTACAATGCC AAACACGAAA CAGTAAATGT GCCAGGTACG
      LeuGluIle TyrLeuIle ArgTyrAsnAla LysHisGlu ThrValAsn ValProGlyThr

2341  GGTTCCTTAT GGCCGCTTTC AGCCCCAAGT CCAATCGGAA AATGTGCCCA TCATTCCCAT
      GlySerLeu TrpProLeu SerAlaProSer ProIleGly LysCysAla HisHisSerHis

2401  CATTTCTCCT TGGACATTGA TGTTGGATGT ACAGACTTAA ATGAGGACTT AGGTGTATGG
      HisPheSer LeuAspIle AspValGlyCys ThrAspLeu AsnGluAsp LeuGlyValTrp

2461  GTGATATTCA AGATTAAGAC GCAAGATGGC CATGCAAGAC TAGGAAATCT AGAATTTCTC
      ValIlePhe LysIleLys ThrGlnAspGly HisAlaArg LeuGlyAsn LeuGluPheLeu

2521  GAAGAGAAAC CATTAGTAGG AGAAGCACTA GCTCGTGTGA AAAGAGCGGA GAAAAAATGG
      GluGluLys ProLeuVal GlyGluAlaLeu AlaArgVal LysArgAla GluLysLysTrp

2581  AGAGACAAAC GTGAAAAATT GGAATGGGAA ACAAATATTG TTTATAAAGA GGCAAAAGAA
      ArgAspLys ArgGluLys LeuGluTrpGlu ThrAsnIle ValTyrLys GluAlaLysGlu

2641  TCTGTAGATG CTTTATTTGT AAACTCTCAA TATGATAGAT TACAAGCGGA TACCAACATC
      SerValAsp AlaLeuPhe ValAsnSerGln TyrAspArg LeuGlnAla AspThrAsnIle

2701  GCGATGATTC ATGCGGCAGA TAAACGCGTT CATAGCATTC GAGAAGCTTA TCTGCCTGAG
      Ala e Ile HisAlaAla AspLysArgVal HisSerIle ArgGluAla TyrLeuProGlu

2761  CTGTCTGTGA TTCCGGGTGT CAATGCGGCT ATTTTTGAAG AATTAGAAGG GCGTATTTTC
      LeuSerVal IleProGly ValAsnAlaAla IlePheGlu GluLeuGlu GlyArgIlePhe

2821  ACTGCATTCT CCCTATATGA TGCGAGAAAT GTCATTAAAA ATGGTGATTT TAATAATGGC
      ThrAlaPhe SerLeuTyr AspAlaArgAsn ValIleLys AsnGlyAsp PheAsnAsnGly
```

09508452 - 141204

Fig. 7D

```
2881  TTATCCTGCT GGAACGTGAA AGGGCATGTA GATGTAGAAG AACAAAACAA CCACCGTTCG
      LeuSerCys TrpAsnVal LysGlyHisVal AspValGlu GluGlnAsn AsnHisArgSer

2941  GTCCTTGTTG TTCCGGAATG GGAAGCAGAA GTGTCACAAG AAGTTCGTGT CTGTCCGGGT
      ValLeuVal ValProGlu TrpGluAlaGlu ValSerGln GluValArg ValCysProGly

3001  CGTGGCTATA TCCTTCGTGT CACAGCGTAC AAGGAGGGAT ATGGAGAAGG TTGCGTAACC
      ArgGlyTyr IleLeuArg ValThrAlaTyr LysGluGly TyrGlyGlu GlyCysValThr

3061  ATTCATGAGA TCGAGAACAA TACAGACGAA CTGAAGTTTA GCAACTGTGT AGAAGAGGAA
      IleHisGlu IleGluAsn AsnThrAspGlu LeuLysPhe SerAsnCys ValGluGluGlu

3121  GTATATCCAA ACAACACGGT AACGTGTAAT GATTATACTG CGACTCAAGA AGAATATGAG
      ValTyrPro AsnAsnThr ValThrCysAsn AspTyrThr AlaThrGln GluGluTyrGlu

3181  GGTACGTACA CTTCTCGTAA TCGAGGATAT GACGGAGCCT ATGAAAGCAA TTCTTCTGTA
      GlyThrTyr ThrSerArg AsnArgGlyTyr AspGlyAla TyrGluSer AsnSerSerVal

3241  CCAGCTGATT ATGCATCAGC CTATGAAGAA AAAGCATATA CAGATGGACG AAGAGACAAT
      ProAlaAsp TyrAlaSer AlaTyrGluGlu LysAlaTyr ThrAspGly ArgArgAspAsn

3301  CCTTGTGAAT CTAACAGAGG ATATGGGGAT TACACACCAC TACCAGCTGG CTATGTGACA
      ProCysGlu SerAsnArg GlyTyrGlyAsp TyrThrPro LeuProAla GlyTyrValThr

3361  AAAGAATTAG AGTACTTCCC AGAAACCGAT AAGGTATGGA TTGAGATCGG AGAAACGGAA
      LysGluLeu GluTyrPhe ProGluThrAsp LysValTrp IleGluIle GlyGluThrGlu

3421  GGAACATTCA TCGTGGACAG CGTGGAATTA CTTCTTATGG AGGAATAA
      GlyThrPhe IleValAsp SerValGluLeu LeuLeuMet GluGlu---
```

EP 0 998 564 B1

T002TT 29h38660

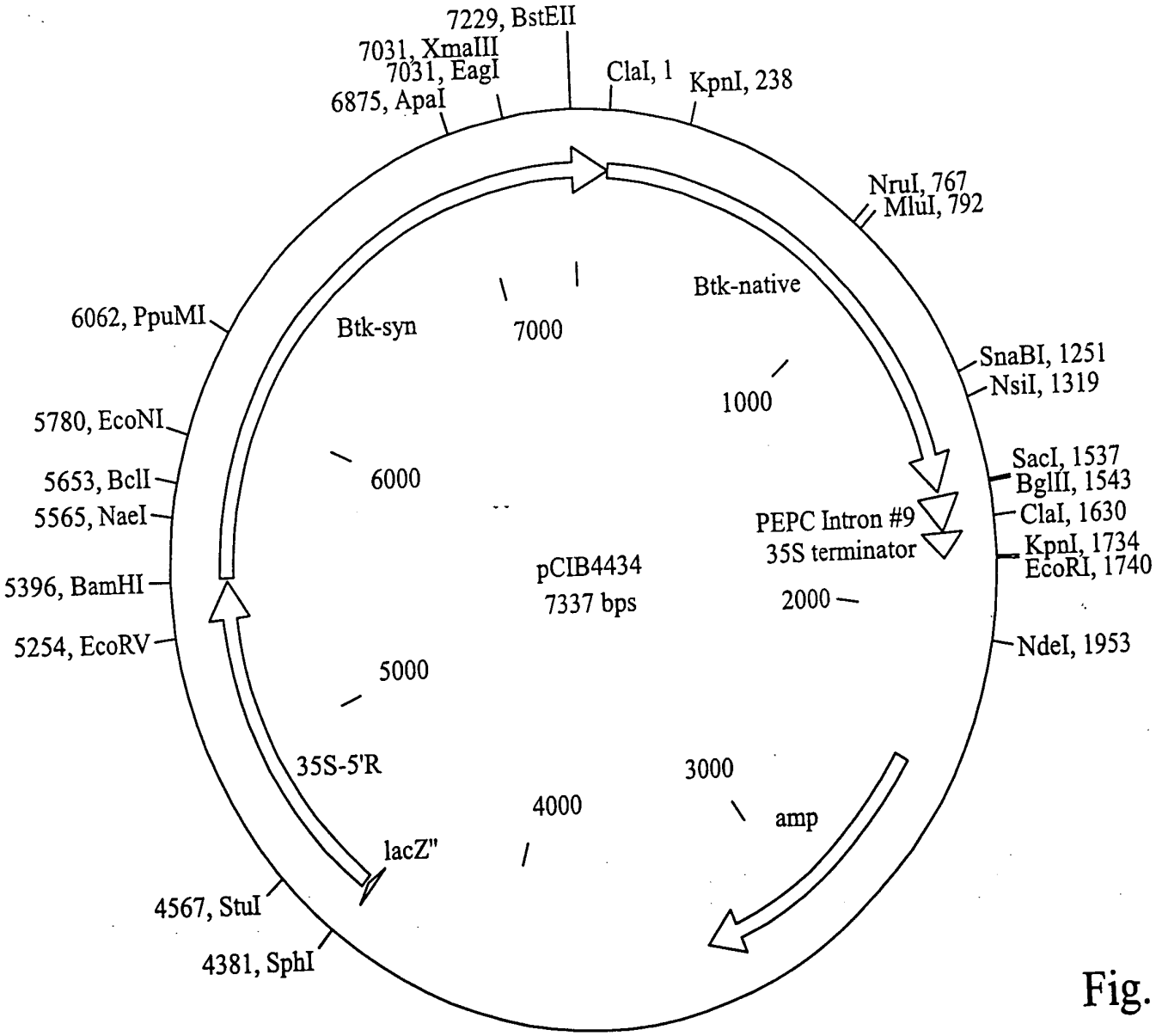


Fig. 8

Fig. 9A

```
   1 ATGGACAACA ACCCCAACAT CAACGAGTGC ATCCCCTACA ACTGCCTGAG CAACCCCGAG
     MetAspAsn AsnProAsn IleAsnGluCys IleProTyr AsnCysLeu SerAsnProGlu

  61 GTGGAGGTGC TGGGCGGCGA GCGCATCGAG ACCGGCTACA CCCCCATCGA CATCAGCCTG
     ValGluVal LeuGlyGly GluArgIleGlu ThrGlyTyr ThrProIle AspIleSerLeu

 121 AGCCTGACCC AGTTCCTGCT GAGCGAGTTC GTGCCCGGCG CCGGCTTCGT GCTGGGCCTG
     SerLeuThr GlnPheLeu LeuSerGluPhe ValProGly AlaGlyPhe ValLeuGlyLeu

 181 GTGGACATCA TCTGGGGCAT CTTCGGCCCC AGCCAGTGGG ACGCCTTCCT GGTGCAGATC
     ValAspIle IleTrpGly IlePheGlyPro SerGlnTrp AspAlaPhe LeuValGlnIle

 241 GAGCAGCTGA TCAACCAGCG CATCGAGGAG TTCGCCCGCA ACCAGGCCAT CAGCCGCCTG
     GluGlnLeu IleAsnGln ArgIleGluGlu PheAlaArg AsnGlnAla IleSerArgLeu

 301 GAGGGCCTGA GCAACCTGTA CCAAATCTAC GCCGAGAGCT TCCGCGAGTG GGAGGCCGAC
     GluGlyLeu SerAsnLeu TyrGlnIleTyr AlaGluSer PheArgGlu TrpGluAlaAsp

 361 CCCACCAACC CCGCCCTGCG CGAGGAGATG CGCATCCAGT TCAACGACAT GAACAGCGCC
     ProThrAsn ProAlaLeu ArgGluGluMet ArgIleGln PheAsnAsp MetAsnSerAla

 421 CTGACCACCG CCATCCCCCT GTTCGCCGTG CAGAACTACC AGGTGCCCCT GCTGAGCGTG
     LeuThrThr AlaIlePro LeuPheAlaVal GlnAsnTyr GlnValPro LeuLeuSerVal

 481 TACGTGCAGG CCGCCAACCT GCACCTGAGC GTGCTGCGCG ACGTCAGCGT GTTCGGCCAG
     TyrValGln AlaAlaAsn LeuHisLeuSer ValLeuArg AspValSer ValPheGlyGln

 541 CGCTGGGGCT TCGACGCCGC CACCATCAAC AGCCGCTACA ACGACCTGAC CCGCCTGATC
     ArgTrpGly PheAspAla AlaThrIleAsn SerArgTyr AsnAspLeu ThrArgLeuIle

 601 GGCAACTACA CCGACCACGC CGTGCGCTGG TACAACACCG GCCTGGAGCG CGTGTGGGGT
     GlyAsnTyr ThrAspHis AlaValArgTrp TyrAsnThr GlyLeuGlu ArgValTrpGly

 661 CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTG
     ProAspSer ArgAspTrp IleArgTyrAsn GlnPheArg ArgGluLeu ThrLeuThrVal

 721 CTGGACATCG TGAGCCTGTT CCCCAACTAC GACAGCCGCA CCTACCCCAT CCGCACCGTG
     LeuAspIle ValSerLeu PheProAsnTyr AspSerArg ThrTyrPro IleArgThrVal

 781 AGCCAGCTGA CCCGCGAGAT TTACACCAAC CCCGTGCTGG AGAACTTCGA CGGCAGCTTC
     SerGlnLeu ThrArgGlu IleTyrThrAsn ProValLeu GluAsnPhe AspGlySerPhe

 841 CGCGGCAGCG CCCAGGGCAT CGAGGGCAGC ATCCGCAGCC CCCACCTGAT GGACATCCTG
     ArgGlySer AlaGlnGly IleGluGlySer IleArgSer ProHisLeu MetAspIleLeu

 901 AACAGCATCA CCATCTACAC CGACGCCCAC CGCGGCGAGT ACTACTGGAG CGGCCACCAG
     AsnSerIle ThrIleTyr ThrAspAlaHis ArgGlyGlu TyrTyrTrp SerGlyHisGln

 961 ATCATGGCCA GCCCCGTCGG CTTCAGCGGC CCCGAGTTCA CCTTCCCCCT GTACGGCACC
     IleMetAla SerProVal GlyPheSerGly ProGluPhe ThrPhePro LeuTyrGlyThr
```

US 6,686,452 - 11/2004

Fig. 9B

```
1021 ATGGGCAACG CTGCACCTCA GCAGCGCATC GTGGCACAGC TGGGCCAGGG AGTGTACCGC
     MetGlyAsn AlaAlaPro GlnGlnArgIle ValAlaGln LeuGlyGln GlyValTyrArg

1081 ACCCTGAGCA GCACCCTGTA CCGTCGACCT TTCAACATCG GCATCAACAA CCAGCAGCTG
     ThrLeuSer SerThrLeu TyrArgArgPro PheAsnIle GlyIleAsn AsnGlnGlnLeu

1141 AGCGTGCTGG ACGGCACCGA GTTCGCCTAC GGCACCAGCA GCAACCTGCC CAGCGCCGTG
     SerValLeu AspGlyThr GluPheAlaTyr GlyThrSer SerAsnLeu ProSerAlaVal

1201 TACCGCAAGA GCGGCACCGT GGACAGCCTG GACGAGATCC CCCCTCAGAA CAACAACGTG
     TyrArgLys SerGlyThr ValAspSerLeu AspGluIle ProProGln AsnAsnAsnVal

1261 CCACCTCGAC AGGGCTTCAG CCACCGTCTG AGCCACGTGA GCATGTTCCG CAGTGGCTTC
     ProProArg GlnGlyPhe SerHisArgLeu SerHisVal SerMetPhe ArgSerGlyPhe

1321 AGCAACAGCA GCGTGAGCAT CATCCGTGCA CCTATGTTCA GCTGGATTCA CCGCAGTGCC
     SerAsnSer SerValSer IleIleArgAla ProMetPhe SerTrpIle HisArgSerAla

1381 GAGTTCAACA ACATCATCCC CAGCAGCCAG ATCACCCAGA TCCCCCTGAC CAAGAGCACC
     GluPheAsn AsnIleIle ProSerSerGln IleThrGln IleProLeu ThrLysSerThr

1441 AACCTGGGCA GCGGCACCAG CGTGGTGAAG GGCCCCGGCT TCACCGGCGG CGACATCCTG
     AsnLeuGly SerGlyThr SerValValLys GlyProGly PheThrGly GlyAspIleLeu

1501 CGCCGCACCA GCCCCGGCCA GATCAGCACC CTGCGCGTGA ACATCACCGC CCCCCTGAGC
     ArgArgThr SerProGly GlnIleSerThr LeuArgVal AsnIleThr AlaProLeuSer

1561 CAGCGCTACC GCGTCCGCAT CCGCTACGCC AGCACCACCA ACCTGCAGTT CCACACCAGC
     GlnArgTyr ArgValArg IleArgTyrAla SerThrThr AsnLeuGln PheHisThrSer

1621 ATCGACGGCC GCCCCATCAA CCAGGGCAAC TTCAGCGCCA CCATGAGCAG CGGCAGCAAC
     IleAspGly ArgProIle AsnGlnGlyAsn PheSerAla ThrMetSer SerGlySerAsn

1681 CTGCAGAGCG GCAGCTTCCG CACCGTGGGC TTCACCACCC CCTTCAACTT CAGCAACGGC
     LeuGlnSer GlySerPhe ArgThrValGly PheThrThr ProPheAsn PheSerAsnGly

1741 AGCAGCGTGT TCACCCTGAG CGCCCACGTG TTCAACAGCG GCAACGAGGT GTACATCGAC
     SerSerVal PheThrLeu SerAlaHisVal PheAsnSer GlyAsnGlu ValTyrIleAsp

1801 CGCATCGAGT TCGTGCCCGC CGAGGTGACC TTCGAGGCCG AGTACGACCT GGAGAGGGCT
     ArgIleGlu PheValPro AlaGluValThr PheGluAla GluTyrAsp LeuGluArgAla

1861 CAGAAGGCCG TGAACGAGCT GTTCACCAGC AGCAACCAGA TCGGCCTGAA GACCGACGTG
     GlnLysAla ValAsnGlu LeuPheThrSer SerAsnGln IleGlyLeu LysThrAspVal

1921 ACCGACTACC ACATCGATCA AGTATCCAAT TTAGTTGAGT GTTTATCTGA TGAATTTTGT
     ThrAspTyr HisIleAsp GlnValSerAsn LeuValGlu CysLeuSer AspGluPheCys

1981 CTGGATGAAA AAAAAGAATT GTCCGAGAAA GTCAAACATG CGAAGCGACT TAGTGATGAG
     LeuAspGlu LysLysGlu LeuSerGluLys ValLysHis AlaLysArg LeuSerAspGlu
```

5,589,474 - 5 - 5,589,474

Fig. 9C

```
2041 CGGAATTTAC TTCAAGATCC AAACTTTAGA GGGATCAATA GACAACTAGA CCGTGGCTGG
     ArgAsnLeu LeuGlnAsp ProAsnPheArg GlyIleAsn ArgGlnLeu AspArgGlyTrp

2101 AGAGGAAGTA CGGATATTAC CATCCAAGGA GGCGATGACG TATTCAAAGA GAATTACGTT
     ArgGlySer ThrAspIle ThrIleGlnGly GlyAspAsp ValPheLys GluAsnTyrVal

2161 ACGCTATTGG GTACCTTCGA CGAGTGCTAC CCCACCTACC TGTACCAGAA GATCGACGAG
     ThrLeuLeu GlyThrPhe AspGluCysTyr ProThrTyr LeuTyrGln LysIleAspGlu

2221 AGCAAGCTGA AGGCCTACAC CCGCTACCAG CTGCGCGGCT ACATCGAGGA CAGCCAGGAC
     SerLysLeu LysAlaTyr ThrArgTyrGln LeuArgGly TyrIleGlu AspSerGlnAsp

2281 CTGGAAATCT ACCTGATCCG CTACAACGCC AAGCACGAGA CCGTGAACGT GCCCGGCACC
     LeuGluIle TyrLeuIle ArgTyrAsnAla LysHisGlu ThrValAsn ValProGlyThr

2341 GGCAGCCTGT GGCCCCTGAG CGCCCCCAGC CCCATCGGCA AGTGCGGGGA GCCGAATCGA
     GlySerLeu TrpProLeu SerAlaProSer ProIleGly LysCysGly GluProAsnArg

2401 TGCGCTCCGC ACCTGGAGTG GAACCCGGAC CTAGACTGCA GCTGCAGGGA CGGGGAGAAG
     CysAlaPro HisLeuGlu TrpAsnProAsp LeuAspCys SerCysArg AspGlyGluLys

2461 TGCGCCCACC ACAGCCACCA CTTCAGCCTG GACATCGACG TGGGCTGCAC CGACCTGAAC
     CysAlaHis HisSerHis HisPheSerLeu AspIleAsp ValGlyCys ThrAspLeuAsn

2521 GAGGACCTGG GCGTGTGGGT GATCTTCAAG ATCAAGACCC AGGACGGCCA CGCCCGCCTG
     GluAspLeu GlyValTrp ValIlePheLys IleLysThr GlnAspGly HisAlaArgLeu

2581 GGCAATCTAG AATTTCTCGA AGAGAAACCA TTAGTAGGAG AAGCACTAGC TCGTGTGAAA
     GlyAsnLeu GluPheLeu GluGluLysPro LeuValGly GluAlaLeu AlaArgValLys

2641 AGAGCGGAGA AAAAATGGAG AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATTGTT
     ArgAlaGlu LysLysTrp ArgAspLysArg GluLysLeu GluTrpGlu ThrAsnIleVal

2701 TATAAAGAGG CAAAAGAATC TGTAGATGCT TTATTTGTAA ACTCTCAATA TGATAGATTA
     TyrLysGlu AlaLysGlu SerValAspAla LeuPheVal AsnSerGln TyrAspArgLeu

2761 CAAGCGGATA CCAACATCGC GATGATTCAT GCGGCAGATA AACGCGTTCA TAGCATTCGA
     GlnAlaAsp ThrAsnIle AlaMetIleHis AlaAlaAsp LysArgVal HisSerIleArg

2821 GAAGCTTATC TGCCTGAGCT GTCTGTGATT CCGGGTGTCA ATGCGGCTAT TTTTGAAGAA
     GluAlaTyr LeuProGlu LeuSerValIle ProGlyVal AsnAlaAla IlePheGluGlu

2881 TTAGAAGGGC GTATTTTCAC TGCATTCTCC CTATATGATG CGAGAAATGT CATTAAAAAT
     LeuGluGly ArgIlePhe ThrAlaPheSer LeuTyrAsp AlaArgAsn ValIleLysAsn

2941 GGTGATTTTA ATAATGGCTT ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA
     GlyAspPhe AsnAsnGly LeuSerCysTrp AsnValLys GlyHisVal AspValGluGlu

3001 CAAAACAACC ACCGTTCGGT CCTTGTTGTT CCGGAATGGG AAGCAGAAGT GTCACAAGAA
     GlnAsnAsn HisArgSer ValLeuValVal ProGluTrp GluAlaGlu ValSerGlnGlu
```

EP 0 464 590 A2

Fig. 9D

```
3061 GTTCGTGTCT GTCCGGGTCG TGGCTATATC CTTCGTGTCA CAGCGTACAA GGAGGGATAT
     ValArgVal CysProGly ArgGlyTyrIle LeuArgVal ThrAlaTyr LysGluGlyTyr

3121 GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAATA CAGACGAACT GAAGTTTAGC
     GlyGluGly CysValThr IleHisGluIle GluAsnAsn ThrAspGlu LeuLysPheSer

3181 AACTGTGTAG AAGAGGAAGT ATATCCAAAC AACACGGTAA CGTGTAATGA TTATACTGCG
     AsnCysVal GluGluGlu ValTyrProAsn AsnThrVal ThrCysAsn AspTyrThrAla

3241 ACTCAAGAAG AATATGAGGG TACGTACACT TCTCGTAATC GAGGATATGA CGGAGCCTAT
     ThrGlnGlu GluTyrGlu GlyThrTyrThr SerArgAsn ArgGlyTyr AspGlyAlaTyr

3301 GAAAGCAATT CTTCTGTACC AGCTGATTAT GCATCAGCCT ATGAAGAAAA AGCATATACA
     GluSerAsn SerSerVal ProAlaAspTyr AlaSerAla TyrGluGlu LysAlaTyrThr

3361 GATGGACGAA GAGACAATCC TTGTGAATCT AACAGAGGAT ATGGGGATTA CACACCACTA
     AspGlyArg ArgAspAsn ProCysGluSer AsnArgGly TyrGlyAsp TyrThrProLeu

3421 CCAGCTGGCT ATGTGACAAA AGAATTAGAG TACTTCCCAG AAACCGATAA GGTATGGATT
     ProAlaGly TyrValThr LysGluLeuGlu TyrPhePro GluThrAsp LysValTrpIle

3481 GAGATCGGAG AAACGGAAGG AACATTCATC GTGGACAGCG TGGAATTACT TCTTATGGAG
     GluIleGly GluThrGlu GlyThrPheIle ValAspSer ValGluLeu LeuLeuMetGlu

3541 GAATAA
     Glu---
```

09884502 - 4TC2T

T0021T" 29h88660

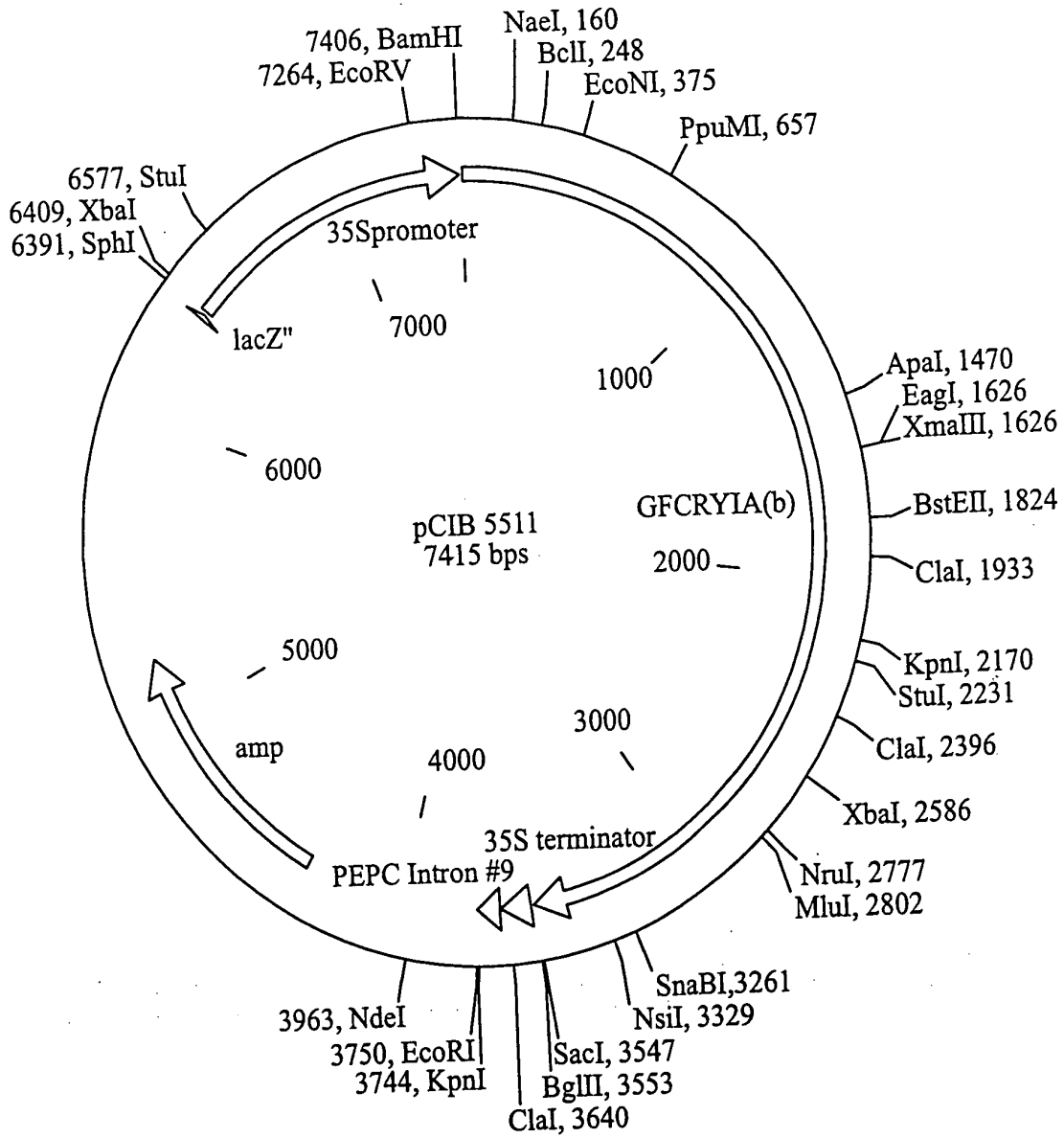


Fig. 10

Fig. 11A

```
   1  ATGGACAACA ACCCCAACAT CAACGAGTGC ATCCCCTACA ACTGCCTGAG CAACCCCGAG
      MetAspAsn AsnProAsn IleAsnGluCys IleProTyr AsnCysLeu SerAsnProGlu

  61  GTGGAGGTGC TGGGCGGCGA GCGCATCGAG ACCGGCTACA CCCCCATCGA CATCAGCCTG
      ValGluVal LeuGlyGly GluArgIleGlu ThrGlyTyr ThrProIle AspIleSerLeu

 121  AGCCTGACCC AGTTCCTGCT GAGCGAGTTC GTGCCCGGCG CCGGCTTCGT GCTGGGCCTG
      SerLeuThr GlnPheLeu LeuSerGluPhe ValProGly AlaGlyPhe ValLeuGlyLeu

 181  GTGGACATCA TCTGGGGCAT CTTCGGCCCC AGCCAGTGGG ACGCCTTCCT GGTGCAGATC
      ValAspIle IleTrpGly IlePheGlyPro SerGlnTrp AspAlaPhe LeuValGlnIle

 241  GAGCAGCTGA TCAACCAGCG CATCGAGGAG TTCGCCCGCA ACCAGGCCAT CAGCCGCCTG
      GluGlnLeu IleAsnGln ArgIleGluGlu PheAlaArg AsnGlnAla IleSerArgLeu

 301  GAGGGCCTGA GCAACCTGTA CCAAATCTAC GCCGAGAGCT TCCGCGAGTG GGAGGCCGAC
      GluGlyLeu SerAsnLeu TyrGlnIleTyr AlaGluSer PheArgGlu TrpGluAlaAsp

 361  CCCACCAACC CCGCCCTGCG CGAGGAGATG CGCATCCAGT TCAACGACAT GAACAGCGCC
      ProThrAsn ProAlaLeu ArgGluGluMet ArgIleGln PheAsnAsp MetAsnSerAla

 421  CTGACCACCG CCATCCCCCT GTTCGCCGTG CAGAACTACC AGGTGCCCCT GCTGAGCGTG
      LeuThrThr AlaIlePro LeuPheAlaVal GlnAsnTyr GlnValPro LeuLeuSerVal

 481  TACGTGCAGG CCGCCAACCT GCACCTGAGC GTGCTGCGCG ACGTCAGCGT GTTCGGCCAG
      TyrValGln AlaAlaAsn LeuHisLeuSer ValLeuArg AspValSer ValPheGlyGln

 541  CGCTGGGGCT TCGACGCCGC CACCATCAAC AGCCGCTACA ACGACCTGAC CCGCCTGATC
      ArgTrpGly PheAspAla AlaThrIleAsn SerArgTyr AsnAspLeu ThrArgLeuIle

 601  GGCAACTACA CCGACCACGC CGTGCGCTGG TACAACACCG GCCTGGAGCG CGTGTGGGGT
      GlyAsnTyr ThrAspHis AlaValArgTrp TyrAsnThr GlyLeuGlu ArgValTrpGly

 661  CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTG
      ProAspSer ArgAspTrp IleArgTyrAsn GlnPheArg ArgGluLeu ThrLeuThrVal

 721  CTGGACATCG TGAGCCTGTT CCCCAACTAC GACAGCCGCA CCTACCCCAT CCGCACCGTG
      LeuAspIle ValSerLeu PheProAsnTyr AspSerArg ThrTyrPro IleArgThrVal

 781  AGCCAGCTGA CCCGCGAGAT TTACACCAAC CCCGTGCTGG AGAACTTCGA CGGCAGCTTC
      SerGlnLeu ThrArgGlu IleTyrThrAsn ProValLeu GluAsnPhe AspGlySerPhe

 841  CGCGGCAGCG CCCAGGGCAT CGAGGGCAGC ATCCGCAGCC CCCACCTGAT GGACATCCTG
      ArgGlySer AlaGlnGly IleGluGlySer IleArgSer ProHisLeu MetAspIleLeu

 901  AACAGCATCA CCATCTACAC CGACGCCCAC CGCGGCGAGT ACTACTGGAG CGGCCACCAG
      AsnSerIle ThrIleTyr ThrAspAlaHis ArgGlyGlu TyrTyrTrp SerGlyHisGln

 961  ATCATGGCCA GCCCCGTCGG CTTCAGCGGC CCCGAGTTCA CCTTCCCCCT GTACGGCACC
      IleMetAla SerProVal GlyPheSerGly ProGluPhe ThrPhePro LeuTyrGlyThr
```

US 6,063,947 - 14 May 2000

Fig. 11B

```
1021  ATGGGCAACG CTGCACCTCA GCAGCGCATC GTGGCACAGC TGGGCCAGGG AGTGTACCGC
      MetGlyAsn AlaAlaPro GlnGlnArgIle ValAlaGln LeuGlyGln GlyValTyrArg

1081  ACCCTGAGCA GCACCCTGTA CCGTCGACCT TTCAACATCG GCATCAACAA CCAGCAGCTG
      ThrLeuSer SerThrLeu TyrArgArgPro PheAsnIle GlyIleAsn AsnGlnGlnLeu

1141  AGCGTGCTGG ACGGCACCGA GTTCGCCTAC GGCACCAGCA GCAACCTGCC CAGCGCCGTG
      SerValLeu AspGlyThr GluPheAlaTyr GlyThrSer SerAsnLeu ProSerAlaVal

1201  TACCGCAAGA GCGGCACCGT GGACAGCCTG GACGAGATCC CCCCTCAGAA CAACAACGTG
      TyrArgLys SerGlyThr ValAspSerLeu AspGluIle ProProGln AsnAsnAsnVal

1261  CCACCTCGAC AGGGCTTCAG CCACCGTCTG AGCCACGTGA GCATGTTCCG CAGTGGCTTC
      ProProArg GlnGlyPhe SerHisArgLeu SerHisVal SerMetPhe ArgSerGlyPhe

1321  AGCAACAGCA GCGTGAGCAT CATCCGTGCA CCTATGTTCA GCTGGATTCA CCGCAGTGCC
      SerAsnSer SerValSer IleIleArgAla ProMetPhe SerTrpIle HisArgSerAla

1381  GAGTTCAACA ACATCATCCC CAGCAGCCAG ATCACCCAGA TCCCCCTGAC CAAGAGCACC
      GluPheAsn AsnIleIle ProSerSerGln IleThrGln IleProLeu ThrLysSerThr

1441  AACCTGGGCA GCGGCACCAG CGTGGTGAAG GGCCCCGGCT TCACCGGCGG CGACATCCTG
      AsnLeuGly SerGlyThr SerValValLys GlyProGly PheThrGly GlyAspIleLeu

1501  CGCCGCACCA GCCCCGGCCA GATCAGCACC CTGCGCGTGA ACATCACCGC CCCCCTGAGC
      ArgArgThr SerProGly GlnIleSerThr LeuArgVal AsnIleThr AlaProLeuSer

1561  CAGCGCTACC GCGTCCGCAT CCGCTACGCC AGCACCACCA ACCTGCAGTT CCACACCAGC
      GlnArgTyr ArgValArg IleArgTyrAla SerThrThr AsnLeuGln PheHisThrSer

1621  ATCGACGGCC GCCCCATCAA CCAGGGCAAC TTCAGCGCCA CCATGAGCAG CGGCAGCAAC
      IleAspGly ArgProIle AsnGlnGlyAsn PheSerAla ThrMetSer SerGlySerAsn

1681  CTGCAGAGCG GCAGCTTCCG CACCGTGGGC TTCACCACCC CCTTCAACTT CAGCAACGGC
      LeuGlnSer GlySerPhe ArgThrValGly PheThrThr ProPheAsn PheSerAsnGly

1741  AGCAGCGTGT TCACCCTGAG CGCCCACGTG TTCAACAGCG GCAACGAGGT GTACATCGAC
      SerSerVal PheThrLeu SerAlaHisVal PheAsnSer GlyAsnGlu ValTyrIleAsp

1801  CGCATCGAGT TCGTGCCCGC CGAGGTGACC TTCGAGGCCG AGTACGACCT GGAGAGGGCT
      ArgIleGlu PheValPro AlaGluValThr PheGluAla GluTyrAsp LeuGluArgAla

1861  CAGAAGGCCG TGAACGAGCT GTTCACCAGC AGCAACCAGA TCGGCCTGAA GACCGACGTG
      GlnLysAla ValAsnGlu LeuPheThrSer SerAsnGln IleGlyLeu LysThrAspVal

1921  ACCGACTACC ACATCGATCA GGTGAGCAAC CTGGTGGAGT GCTTAAGCGA CGAGTTCTGC
      ThrAspTyr HisIleAsp GlnValSerAsn LeuValGlu CysLeuSer AspGluPheCys

1981  CTGGACGAGA AGAAGGAGCT GAGCGAGAAG GTGAAGCACG CCAAGCGCCT GAGCGACGAG
      LeuAspGlu LysLysGlu LeuSerGluLys ValLysHis AlaLysArg LeuSerAspGlu
```

0950452 - 112001

Fig. 11C

```
2041  CGCAACCTGC TGCAGGACCC CAACTTCCGC GGCATCAACC GCCAGCTGGA CCGCGGCTGG
      ArgAsnLeu LeuGlnAsp ProAsnPheArg GlyIleAsn ArgGlnLeu AspArgGlyTrp

2101  CGAGGCAGCA CCGATATCAC CATCCAGGGC GGCGACGACG TGTTCAAGGA GAACTACGTG
      ArgGlySer ThrAspIle ThrIleGlnGly GlyAspAsp ValPheLys GluAsnTyrVal

2161  ACCCTGCTGG GCACCTTCGA CGAGTGCTAC CCCACCTACC TGTACCAGAA GATCGACGAG
      ThrLeuLeu GlyThrPhe AspGluCysTyr ProThrTyr LeuTyrGln LysIleAspGlu

2221  AGCAAGCTGA AGGCCTACAC CCGCTACCAG CTGCGCGGCT ACATCGAGGA CAGCCAGGAC
      SerLysLeu LysAlaTyr ThrArgTyrGln LeuArgGly TyrIleGlu AspSerGlnAsp

2281  CTGGAAATCT ACCTGATCCG CTACAACGCC AAGCACGAGA CCGTGAACGT GCCCGGCACC
      LeuGluIle TyrLeuIle ArgTyrAsnAla LysHisGlu ThrValAsn ValProGlyThr

2341  GGCAGCCTGT GGCCCCTGAG CGCCCCCAGC CCCATCGGCA AGTGCGGGGA GCCGAATCGA
      GlySerLeu TrpProLeu SerAlaProSer ProIleGly LysCysGly GluProAsnArg

2401  TGCGCTCCGC ACCTGGAGTG GAACCCGGAC CTAGACTGCA GCTGCAGGGA CGGGGAGAAG
      CysAlaPro HisLeuGlu TrpAsnProAsp LeuAspCys SerCysArg AspGlyGluLys

2461  TGCGCCCACC ACAGCCACCA CTTCAGCCTG GACATCGACG TGGGCTGCAC CGACCTGAAC
      CysAlaHis HisSerHis HisPheSerLeu AspIleAsp ValGlyCys ThrAspLeuAsn

2521  GAGGACCTGG GCGTGTGGGT GATCTTCAAG ATCAAGACCC AGGACGGCCA CGCCCGCCTG
      GluAspLeu GlyValTrp ValIlePheLys IleLysThr GlnAspGly HisAlaArgLeu

2581  GGCAATCTAG AATTTCTCGA AGAGAAACCA TTAGTAGGAG AAGCACTAGC TCGTGTGAAA
      GlyAsnLeu GluPheLeu GluGluLysPro LeuValGly GluAlaLeu AlaArgValLys

2641  AGAGCGGAGA AAAAATGGAG AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATTGTT
      ArgAlaGlu LysLysTrp ArgAspLysArg GluLysLeu GluTrpGlu ThrAsnIleVal

2701  TATAAAGAGG CAAAAGAATC TGTAGATGCT TTATTTGTAA ACTCTCAATA TGATAGATTA
      TyrLysGlu AlaLysGlu SerValAspAla LeuPheVal AsnSerGln TyrAspArgLeu

2761  CAAGCGGATA CCAACATCGC GATGATTCAT GCGGCAGATA AACGCGTTCA TAGCATTCGA
      GlnAlaAsp ThrAsnIle AlaMetIleHis AlaAlaAsp LysArgVal HisSerIleArg

2821  GAAGCTTATC TGCCTGAGCT GTCTGTGATT CCGGGTGTCA ATGCGGCTAT TTTTGAAGAA
      GluAlaTyr LeuProGlu LeuSerValIle ProGlyVal AsnAlaAla IlePheGluGlu

2881  TTAGAAGGGC GTATTTTCAC TGCATTCTCC CTATATGATG CGAGAAATGT CATTAAAAAT
      LeuGluGly ArgIlePhe ThrAlaPheSer LeuTyrAsp AlaArgAsn ValIleLysAsn

2941  GGTGATTTTA ATAATGGCTT ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA
      GlyAspPhe AsnAsnGly LeuSerCysTrp AsnValLys GlyHisVal AspValGluGlu

3001  CAAAACAACC ACCGTTCGGT CCTTGTTGTT CCGGAATGGG AAGCAGAAGT GTCACAAGAA
      GlnAsnAsn HisArgSer ValLeuValVal ProGluTrp GluAlaGlu ValSerGlnGlu
```

09682462 - 112004

Fig. 11D

```
3061  GTTCGTGTCT GTCCGGGTCG TGGCTATATC CTTCGTGTCA CAGCGTACAA GGAGGGATAT
      ValArgVal CysProGly ArgGlyTyrIle LeuArgVal ThrAlaTyr LysGluGlyTyr

3121  GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAATA CAGACGAACT GAAGTTTAGC
      GlyGluGly CysValThr IleHisGluIle GluAsnAsn ThrAspGlu LeuLysPheSer

3181  AACTGTGTAG AAGAGGAAGT ATATCCAAAC AACACGGTAA CGTGTAATGA TTATACTGCG
      AsnCysVal GluGluGlu ValTyrProAsn AsnThrVal ThrCysAsn AspTyrThrAla

3241  ACTCAAGAAG AATATGAGGG TACGTACACT TCTCGTAATC GAGGATATGA CGGAGCCTAT
      ThrGlnGlu GluTyrGlu GlyThrTyrThr SerArgAsn ArgGlyTyr AspGlyAlaTyr

3301  GAAAGCAATT CTTCTGTACC AGCTGATTAT GCATCAGCCT ATGAAGAAAA AGCATATACA
      GluSerAsn SerSerVal ProAlaAspTyr AlaSerAla TyrGluGlu LysAlaTyrThr

3361  GATGGACGAA GAGACAATCC TTGTGAATCT AACAGAGGAT ATGGGGATTA CACACCACTA
      AspGlyArg ArgAspAsn ProCysGluSer AsnArgGly TyrGlyAsp TyrThrProLeu

3421  CCAGCTGGCT ATGTGACAAA AGAATTAGAG TACTTCCCAG AAACCGATAA GGTATGGATT
      ProAlaGly TyrValThr LysGluLeuGlu TyrPhePro GluThrAsp LysValTrpIle

3481  GAGATCGGAG AAACGGAAGG AACATTCATC GTGGACAGCG TGGAATTACT TCTTATGGAG
      GluIleGly GluThrGlu GlyThrPheIle ValAspSer ValGluLeu LeuLeuMetGlu

3541  GAATAA
      Glu---
```

4,925,795 - 15 - May 29, 1990

TOZTT"29h88660

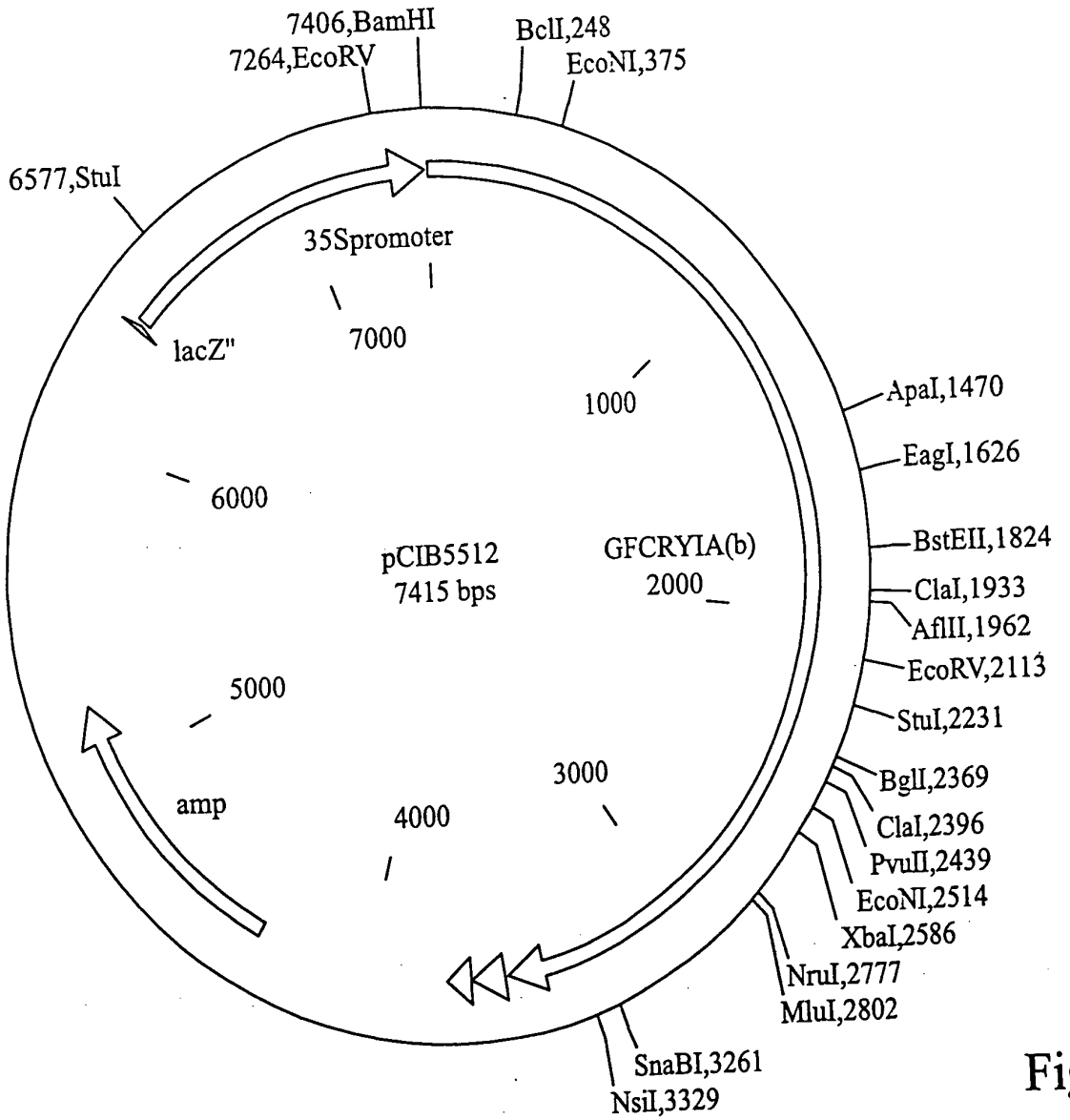


Fig. 12

Fig. 13A

```
1    ATGGACAACA ACCCCAACAT CAACGAGTGC ATCCCCTACA ACTGCCTGAG CAACCCCGAG
     MetAspAsn AsnProAsn IleAsnGluCys IleProTyr AsnCysLeu SerAsnProGlu

61   GTGGAGGTGC TGGGCGGCGA GCGCATCGAG ACCGGCTACA CCCCCATCGA CATCAGCCTG
     ValGluVal LeuGlyGly GluArgIleGlu ThrGlyTyr ThrProIle AspIleSerLeu

121  AGCCTGACCC AGTTCCTGCT GAGCGAGTTC GTGCCCGGCG CCGGCTTCGT GCTGGGCCTG
     SerLeuThr GlnPheLeu LeuSerGluPhe ValProGly AlaGlyPhe ValLeuGlyLeu

181  GTGGACATCA TCTGGGGCAT CTTCGGCCCC AGCCAGTGGG ACGCCTTCCT GGTGCAGATC
     ValAspIle IleTrpGly IlePheGlyPro SerGlnTrp AspAlaPhe LeuValGlnIle

241  GAGCAGCTGA TCAACCAGCG CATCGAGGAG TTCGCCCGCA ACCAGGCCAT CAGCCGCCTG
     GluGlnLeu IleAsnGln ArgIleGluGlu PheAlaArg AsnGlnAla IleSerArgLeu

301  GAGGGCCTGA GCAACCTGTA CCAAATCTAC GCCGAGAGCT TCCGCGAGTG GGAGGCCGAC
     GluGlyLeu SerAsnLeu TyrGlnIleTyr AlaGluSer PheArgGlu TrpGluAlaAsp

361  CCCACCAACC CCGCCCTGCG CGAGGAGATG CGCATCCAGT TCAACGACAT GAACAGCGCC
     ProThrAsn ProAlaLeu ArgGluGluMet ArgIleGln PheAsnAsp MetAsnSerAla

421  CTGACCACCG CCATCCCCCT GTTCGCCGTG CAGAACTACC AGGTGCCCCT GCTGAGCGTG
     LeuThrThr AlaIlePro LeuPheAlaVal GlnAsnTyr GlnValPro LeuLeuSerVal

481  TACGTGCAGG CCGCCAACCT GCACCTGAGC GTGCTGCGCG ACGTCAGCGT GTTCGGCCAG
     TyrValGln AlaAlaAsn LeuHisLeuSer ValLeuArg AspValSer ValPheGlyGln

541  CGCTGGGGCT TCGACGCCGC CACCATCAAC AGCCGCTACA ACGACCTGAC CCGCCTGATC
     ArgTrpGly PheAspAla AlaThrIleAsn SerArgTyr AsnAspLeu ThrArgLeuIle

601  GGCAACTACA CCGACCACGC CGTGCGCTGG TACAACACCG GCCTGGAGCG CGTGTGGGGT
     GlyAsnTyr ThrAspHis AlaValArgTrp TyrAsnThr GlyLeuGlu ArgValTrpGly

661  CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTG
     ProAspSer ArgAspTrp IleArgTyrAsn GlnPheArg ArgGluLeu ThrLeuThrVal

721  CTGGACATCG TGAGCCTGTT CCCCAACTAC GACAGCCGCA CCTACCCCAT CCGCACCGTG
     LeuAspIle ValSerLeu PheProAsnTyr AspSerArg ThrTyrPro IleArgThrVal

781  AGCCAGCTGA CCCGCGAGAT TTACACCAAC CCCGTGCTGG AGAACTTCGA CGGCAGCTTC
     SerGlnLeu ThrArgGlu IleTyrThrAsn ProValLeu GluAsnPhe AspGlySerPhe

841  CGCGGCAGCG CCCAGGGCAT CGAGGGCAGC ATCCGCAGCC CCCACCTGAT GGACATCCTG
     ArgGlySer AlaGlnGly IleGluGlySer IleArgSer ProHisLeu MetAspIleLeu

901  AACAGCATCA CCATCTACAC CGACGCCCAC CGCGGCGAGT ACTACTGGAG CGGCCACCAG
     AsnSerIle ThrIleTyr ThrAspAlaHis ArgGlyGlu TyrTyrTrp SerGlyHisGln

961  ATCATGGCCA GCCCCGTCGG CTTCAGCGGC CCCGAGTTCA CCTTCCCCCT GTACGGCACC
     IleMetAla SerProVal GlyPheSerGly ProGluPhe ThrPhePro LeuTyrGlyThr
```

Sequence: 1-1020

Fig. 13B

```
1021  ATGGGCAACG CTGCACCTCA GCAGCGCATC GTGGCACAGC TGGGCCAGGG AGTGTACCGC
      MetGlyAsn AlaAlaPro GlnGlnArgIle ValAlaGln LeuGlyGln GlyValTyrArg

1081  ACCCTGAGCA GCACCCTGTA CCGTCGACCT TTCAACATCG GCATCAACAA CCAGCAGCTG
      ThrLeuSer SerThrLeu TyrArgArgPro PheAsnIle GlyIleAsn AsnGlnGlnLeu

1141  AGCGTGCTGG ACGGCACCGA GTTCGCCTAC GGCACCAGCA GCAACCTGCC CAGCGCCGTG
      SerValLeu AspGlyThr GluPheAlaTyr GlyThrSer SerAsnLeu ProSerAlaVal

1201  TACCGCAAGA GCGGCACCGT GGACAGCCTG GACGAGATCC CCCCTCAGAA CAACAACGTG
      TyrArgLys SerGlyThr ValAspSerLeu AspGluIle ProProGln AsnAsnAsnVal

1261  CCACCTCGAC AGGGCTTCAG CCACCGTCTG AGCCACGTGA GCATGTTCCG CAGTGGCTTC
      ProProArg GlnGlyPhe SerHisArgLeu SerHisVal SerMetPhe ArgSerGlyPhe

1321  AGCAACAGCA GCGTGAGCAT CATCCGTGCA CCTATGTTCA GCTGGATTCA CCGCAGTGCC
      SerAsnSer SerValSer IleIleArgAla ProMetPhe SerTrpIle HisArgSerAla

1381  GAGTTCAACA ACATCATCCC CAGCAGCCAG ATCACCCAGA TCCCCCTGAC CAAGAGCACC
      GluPheAsn AsnIleIle ProSerSerGln IleThrGln IleProLeu ThrLysSerThr

1441  AACCTGGGCA GCGGCACCAG CGTGGTGAAG GGCCCCGGCT TCACCGGCGG CGACATCCTG
      AsnLeuGly SerGlyThr SerValValLys GlyProGly PheThrGly GlyAspIleLeu

1501  CGCCGCACCA GCCCCGGCCA GATCAGCACC CTGCGCGTGA ACATCACCGC CCCCCTGAGC
      ArgArgThr SerProGly GlnIleSerThr LeuArgVal AsnIleThr AlaProLeuSer

1561  CAGCGCTACC GCGTCCGCAT CCGCTACGCC AGCACCACCA ACCTGCAGTT CCACACCAGC
      GlnArgTyr ArgValArg IleArgTyrAla SerThrThr AsnLeuGln PheHisThrSer

1621  ATCGACGGCC GCCCCATCAA CCAGGGCAAC TTCAGCGCCA CCATGAGCAG CGGCAGCAAC
      IleAspGly ArgProIle AsnGlnGlyAsn PheSerAla ThrMetSer SerGlySerAsn

1681  CTGCAGAGCG GCAGCTTCCG CACCGTGGGC TTCACCACCC CCTTCAACTT CAGCAACGGC
      LeuGlnSer GlySerPhe ArgThrValGly PheThrThr ProPheAsn PheSerAsnGly

1741  AGCAGCGTGT TCACCCTGAG CGCCCACGTG TTCAACAGCG GCAACGAGGT GTACATCGAC
      SerSerVal PheThrLeu SerAlaHisVal PheAsnSer GlyAsnGlu ValTyrIleAsp

1801  CGCATCGAGT TCGTGCCCGC CGAGGTGACC TTCGAGGCCG AGTACGACCT GGAGAGGGCT
      ArgIleGlu PheValPro AlaGluValThr PheGluAla GluTyrAsp LeuGluArgAla

1861  CAGAAGGCCG TGAACGAGCT GTTCACCAGC AGCAACCAGA TCGGCCTGAA GACCGACGTG
      GlnLysAla ValAsnGlu LeuPheThrSer SerAsnGln IleGlyLeu LysThrAspVal

1921  ACCGACTACC ACATCGATCA GGTGAGCAAC CTGGTGGAGT GCTTAAGCGA CGAGTTCTGC
      ThrAspTyr HisIleAsp GlnValSerAsn LeuValGlu CysLeuSer AspGluPheCys

1981  CTGGACGAGA AGAAGGAGCT GAGCGAGAAG GTGAAGCACG CCAAGCGCCT GAGCGACGAG
      LeuAspGlu LysLysGlu LeuSerGluLys ValLysHis AlaLysArg LeuSerAspGlu
```

US 6,063,947

Fig. 13C

```
2041  CGCAACCTGC TGCAGGACCC CAACTTCCGC GGCATCAACC GCCAGCTGGA CCGCGGCTGG
      ArgAsnLeu LeuGlnAsp ProAsnPheArg GlyIleAsn ArgGlnLeu AspArgGlyTrp

2101  CGAGGCAGCA CCGATATCAC CATCCAGGGC GGCGACGACG TGTTCAAGGA GAACTACGTG
      ArgGlySer ThrAspIle ThrIleGlnGly GlyAspAsp ValPheLys GluAsnTyrVal

2161  ACCCTGCTGG GCACCTTCGA CGAGTGCTAC CCCACCTACC TGTACCAGAA GATCGACGAG
      ThrLeuLeu GlyThrPhe AspGluCysTyr ProThrTyr LeuTyrGln LysIleAspGlu

2221  AGCAAGCTGA AGGCCTACAC CCGCTACCAG CTGCGCGGCT ACATCGAGGA CAGCCAGGAC
      SerLysLeu LysAlaTyr ThrArgTyrGln LeuArgGly TyrIleGlu AspSerGlnAsp

2281  CTGGAAATCT ACCTGATCCG CTACAACGCC AAGCACGAGA CCGTGAACGT GCCCGGCACC
      LeuGluIle TyrLeuIle ArgTyrAsnAla LysHisGlu ThrValAsn ValProGlyThr

2341  GGCAGCCTGT GGCCCCTGAG CGCCCCCAGC CCCATCGGCA AGTGCGGGGA GCCGAATCGA
      GlySerLeu TrpProLeu SerAlaProSer ProIleGly LysCysGly GluProAsnArg

2401  TGCGCTCCGC ACCTGGAGTG GAACCCGGAC CTAGACTGCA GCTGCAGGGA CGGGGAGAAG
      CysAlaPro HisLeuGlu TrpAsnProAsp LeuAspCys SerCysArg AspGlyGluLys

2461  TGCGCCCACC ACAGCCACCA CTTCAGCCTG GACATCGACG TGGGCTGCAC CGACCTGAAC
      CysAlaHis HisSerHis HisPheSerLeu AspIleAsp ValGlyCys ThrAspLeuAsn

2521  GAGGACCTGG GCGTGTGGGT GATCTTCAAG ATCAAGACCC AGGACGGCCA CGCCCGCCTG
      GluAspLeu GlyValTrp ValIlePheLys IleLysThr GlnAspGly HisAlaArgLeu

2581  GGCAATCTAG AGTTCCTGGA GGAGAAGCCC CTGGTGGGCG AGGCCCTGGC CCGCGTGAAG
      GlyAsnLeu GluPheLeu GluGluLysPro LeuValGly GluAlaLeu AlaArgValLys

2641  CGCGCCGAGA AGAAGTGGCG CGACAAGCGC GAGAAGCTGG AGTGGGAGAC CAACATCGTG
      ArgAlaGlu LysLysTrp ArgAspLysArg GluLysLeu GluTrpGlu ThrAsnIleVal

2701  TACAAGGAGG CCAAGGAGAG CGTGGACGCC CTGTTCGTGA ACAGCCAGTA CGACCGCCTG
      TyrLysGlu AlaLysGlu SerValAspAla LeuPheVal AsnSerGln TyrAspArgLeu

2761  CAGGCCGACA CCAACATCGC CATGATCCAC GCCGCCGACA AGCGCGTGCA CAGCATTCGC
      GlnAlaAsp ThrAsnIle AlaMetIleHis AlaAlaAsp LysArgVal HisSerIleArg

2821  GAGGCCTACC TGCCCGAGCT GAGCGTGATC CCCGGCGTGA ACGCCGCCAT CTTCGAGGAA
      GluAlaTyr LeuProGlu LeuSerValIle ProGlyVal AsnAlaAla IlePheGluGlu

2881  CTCGAGGGCC GCATCTTCAC CGCCTTCAGC CTGTACGACG CCCGCAACGT GATCAAGAAC
      LeuGluGly ArgIlePhe ThrAlaPheSer LeuTyrAsp AlaArgAsn ValIleLysAsn

2941  GGCGACTTCA ACAACGGCCT GAGCTGCTGG AACGTGAAGG GCCACGTGGA CGTGGAGGAG
      GlyAspPhe AsnAsnGly LeuSerCysTrp AsnValLys GlyHisVal AspValGluGlu

3001  CAGAACAACC ACCGCAGCGT GCTGGTGGTG CCCGAGTGGG AGGCCGAGGT GAGCCAGGAG
      GlnAsnAsn HisArgSer ValLeuValVal ProGluTrp GluAlaGlu ValSerGlnGlu
```

US 6,284,471 B1

Fig. 13D

```
3061  GTGCGCGTGT GCCCCGGCCG CGGCTACATC CTGCGCGTGA CCGCCTACAA GGAGGGCTAC
      ValArgVal CysProGly ArgGlyTyrIle LeuArgVal ThrAlaTyr LysGluGlyTyr

3121  GGCGAGGGCT GCGTGACCAT CCACGAGATC GAGAACAACA CCGACGAGCT CAAGTTCAGC
      GlyGluGly CysValThr IleHisGluIle GluAsnAsn ThrAspGlu LeuLysPheSer

3181  AACTGCGTGG AGGAGGAGGT GTACCCCAAC AACACCGTGA CCTGCAACGA CTACACCGCG
      AsnCysVal GluGluGlu ValTyrProAsn AsnThrVal ThrCysAsn AspTyrThrAla

3241  ACCCAGGAGG AGTACGAGGG CACCTACACC AGCCGCAACC GCGGCTACGA CGGCGCCTAC
      ThrGlnGlu GluTyrGlu GlyThrTyrThr SerArgAsn ArgGlyTyr AspGlyAlaTyr

3301  GAGAGCAACA GCAGCGTGCC CGCCGACTAC GCCAGCGCCT ACGAGGAGAA GGCCTACACC
      GluSerAsn SerSerVal ProAlaAspTyr AlaSerAla TyrGluGlu LysAlaTyrThr

3361  GACGGCCGCC GCGACAACCC CTGCGAGAGC AACCGCGGCT ACGGCGACTA CACCCCCCTG
      AspGlyArg ArgAspAsn ProCysGluSer AsnArgGly TyrGlyAsp TyrThrProLeu

3421  CCCGCCGGCT ACGTGACCAA GGAGCTGGAG TACTTCCCCG AGACCGACAA GGTGTGGATC
      ProAlaGly TyrValThr LysGluLeuGlu TyrPhePro GluThrAsp LysValTrpIle

3481  GAGATCGGCG AGACCGAGGG CACCTTCATC GTGGACAGCG TGGAGCTGCT GCTGATGGAG
      GluIleGly GluThrGlu GlyThrPheIle ValAspSer ValGluLeu LeuLeuMetGlu

3541  GAG
      Glu
```

Docket No. 4150-4

T0027T "29h88660

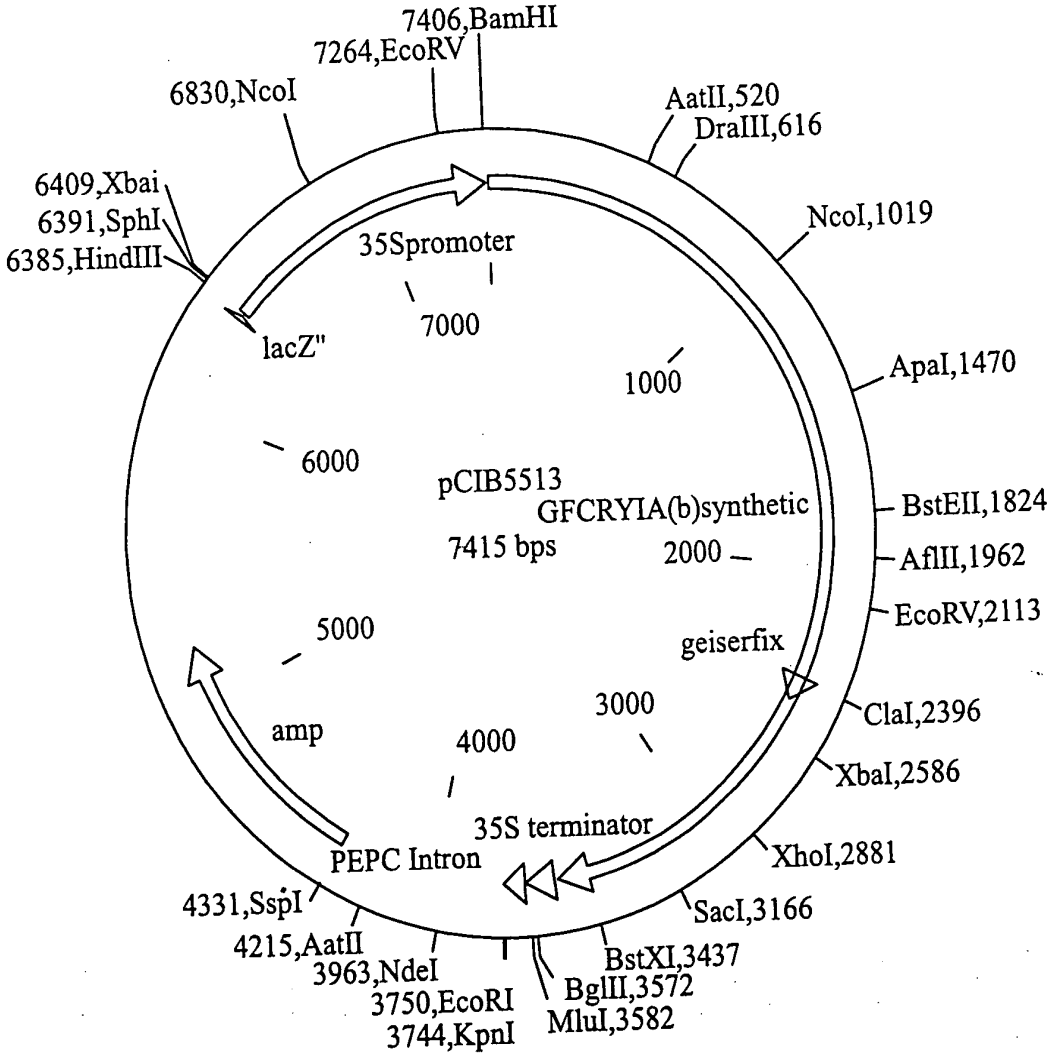


Fig. 14

Fig. 15A

```
1   ATGGACAACA ACCCCAACAT CAACGAGTGC ATCCCCTACA ACTGCCTGAG CAACCCCGAG
    MetAspAsn AsnProAsn IleAsnGluCys IleProTyr AsnCysLeu SerAsnProGlu

61  GTGGAGGTGC TGGGCGGCGA GCGCATCGAG ACCGGCTACA CCCCCATCGA CATCAGCCTG
    ValGluVal LeuGlyGly GluArgIleGlu ThrGlyTyr ThrProIle AspIleSerLeu

121 AGCCTGACCC AGTTCCTGCT GAGCGAGTTC GTGCCCGGCG CCGGCTTCGT GCTGGGCCTG
    SerLeuThr GlnPheLeu LeuSerGluPhe ValProGly AlaGlyPhe ValLeuGlyLeu

181 GTGGACATCA TCTGGGGCAT CTTCGGCCCC AGCCAGTGGG ACGCCTTCCT GGTGCAGATC
    ValAspIle IleTrpGly IlePheGlyPro SerGlnTrp AspAlaPhe LeuValGlnIle

241 GAGCAGCTGA TCAACCAGCG CATCGAGGAG TTCGCCCGCA ACCAGGCCAT CAGCCGCCTG
    GluGlnLeu IleAsnGln ArgIleGluGlu PheAlaArg AsnGlnAla IleSerArgLeu

301 GAGGGCCTGA GCAACCTGTA CCAAATCTAC GCCGAGAGCT TCCGCGAGTG GGAGGCCGAC
    GluGlyLeu SerAsnLeu TyrGlnIleTyr AlaGluSer PheArgGlu TrpGluAlaAsp

361 CCCACCAACC CCGCCCTGCG CGAGGAGATG CGCATCCAGT TCAACGACAT GAACAGCGCC
    ProThrAsn ProAlaLeu ArgGluGluMet ArgIleGln PheAsnAsp MetAsnSerAla

421 CTGACCACCG CCATCCCCCT GTTCGCCGTG CAGAACTACC AGGTGCCCCT GCTGAGCGTG
    LeuThrThr AlaIlePro LeuPheAlaVal GlnAsnTyr GlnValPro LeuLeuSerVal

481 TACGTGCAGG CCGCCAACCT GCACCTGAGC GTGCTGCGCG ACGTCAGCGT GTTCGGCCAG
    TyrValGln AlaAlaAsn LeuHisLeuSer ValLeuArg AspValSer ValPheGlyGln

541 CGCTGGGGCT TCGACGCCGC CACCATCAAC AGCCGCTACA ACGACCTGAC CCGCCTGATC
    ArgTrpGly PheAspAla AlaThrIleAsn SerArgTyr AsnAspLeu ThrArgLeuIle

601 GGCAACTACA CCGACCACGC CGTGCGCTGG TACAACACCG GCCTGGAGCG CGTGTGGGGT
    GlyAsnTyr ThrAspHis AlaValArgTrp TyrAsnThr GlyLeuGlu ArgValTrpGly

661 CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTG
    ProAspSer ArgAspTrp IleArgTyrAsn GlnPheArg ArgGluLeu ThrLeuThrVal

721 CTGGACATCG TGAGCCTGTT CCCCAACTAC GACAGCCGCA CCTACCCCAT CCGCACCGTG
    LeuAspIle ValSerLeu PheProAsnTyr AspSerArg ThrTyrPro IleArgThrVal

781 AGCCAGCTGA CCCGCGAGAT TTACACCAAC CCCGTGCTGG AGAACTTCGA CGGCAGCTTC
    SerGlnLeu ThrArgGlu IleTyrThrAsn ProValLeu GluAsnPhe AspGlySerPhe

841 CGCGGCAGCG CCCAGGGCAT CGAGGGCAGC ATCCGCAGCC CCCACCTGAT GGACATCCTG
    ArgGlySer AlaGlnGly IleGluGlySer IleArgSer ProHisLeu MetAspIleLeu

901 AACAGCATCA CCATCTACAC CGACGCCCAC CGCGGCGAGT ACTACTGGAG CGGCCACCAG
    AsnSerIle ThrIleTyr ThrAspAlaHis ArgGlyGlu TyrTyrTrp SerGlyHisGln

961 ATCATGGCCA GCCCCGTCGG CTTCAGCGGC CCCGAGTTCA CCTTCCCCCT GTACGGCACC
    IleMetAla SerProVal GlyPheSerGly ProGluPhe ThrPhePro LeuTyrGlyThr
```

US 6,329,501 B1

Fig. 15B

```
1021  ATGGGCAACG CTGCACCTCA GCAGCGCATC GTGGCACAGC TGGGCCAGGG AGTGTACCGC
      MetGlyAsn AlaAlaPro GlnGlnArgIle ValAlaGln LeuGlyGln GlyValTyrArg

1081  ACCCTGAGCA GCACCCTGTA CCGTCGACCT TTCAACATCG GCATCAACAA CCAGCAGCTG
      ThrLeuSer SerThrLeu TyrArgArgPro PheAsnIle GlyIleAsn AsnGlnGlnLeu

1141  AGCGTGCTGG ACGGCACCGA GTTCGCCTAC GGCACCAGCA GCAACCTGCC CAGCGCCGTG
      SerValLeu AspGlyThr GluPheAlaTyr GlyThrSer SerAsnLeu ProSerAlaVal

1201  TACCGCAAGA GCGGCACCGT GGACAGCCTG GACGAGATCC CCCCTCAGAA CAACAACGTG
      TyrArgLys SerGlyThr ValAspSerLeu AspGluIle ProProGln AsnAsnAsnVal

1261  CCACCTCGAC AGGGCTTCAG CCACCGTCTG AGCCACGTGA GCATGTTCCG CAGTGGCTTC
      ProProArg GlnGlyPhe SerHisArgLeu SerHisVal SerMetPhe ArgSerGlyPhe

1321  AGCAACAGCA GCGTGAGCAT CATCCGTGCA CCTATGTTCA GCTGGATTCA CCGCAGTGCC
      SerAsnSer SerValSer IleIleArgAla ProMetPhe SerTrpIle HisArgSerAla

1381  GAGTTCAACA ACATCATCCC CAGCAGCCAG ATCACCCAGA TCCCCCTGAC CAAGAGCACC
      GluPheAsn AsnIleIle ProSerSerGln IleThrGln IleProLeu ThrLysSerThr

1441  AACCTGGGCA GCGGCACCAG CGTGGTGAAG GGCCCCGGCT TCACCGGCGG CGACATCCTG
      AsnLeuGly SerGlyThr SerValValLys GlyProGly PheThrGly GlyAspIleLeu

1501  CGCCGCACCA GCCCCGGCCA GATCAGCACC CTGCGCGTGA ACATCACCGC CCCCCTGAGC
      ArgArgThr SerProGly GlnIleSerThr LeuArgVal AsnIleThr AlaProLeuSer

1561  CAGCGCTACC GCGTCCGCAT CCGCTACGCC AGCACCACCA ACCTGCAGTT CCACACCAGC
      GlnArgTyr ArgValArg IleArgTyrAla SerThrThr AsnLeuGln PheHisThrSer

1621  ATCGACGGCC GCCCCATCAA CCAGGGCAAC TTCAGCGCCA CCATGAGCAG CGGCAGCAAC
      IleAspGly ArgProIle AsnGlnGlyAsn PheSerAla ThrMetSer SerGlySerAsn

1681  CTGCAGAGCG GCAGCTTCCG CACCGTGGGC TTCACCACCC CCTTCAACTT CAGCAACGGC
      LeuGlnSer GlySerPhe ArgThrValGly PheThrThr ProPheAsn PheSerAsnGly

1741  AGCAGCGTGT TCACCCTGAG CGCCCACGTG TTCAACAGCG GCAACGAGGT GTACATCGAC
      SerSerVal PheThrLeu SerAlaHisVal PheAsnSer GlyAsnGlu ValTyrIleAsp

1801  CGCATCGAGT TCGTGCCCGC CGAGGTGACC TTCGAGGCCG AGTACGACCT GGAGAGGGCT
      ArgIleGlu PheValPro AlaGluValThr PheGluAla GluTyrAsp LeuGluArgAla

1861  CAGAAGGCCG TGAACGAGCT GTTCACCAGC AGCAACCAGA TCGGCCTGAA GACCGACGTG
      GlnLysAla ValAsnGlu LeuPheThrSer SerAsnGln IleGlyLeu LysThrAspVal

1921  ACCGACTACC ACATCGATCA AGTATCCAAT TTAGTTGAGT GTTTATCTGA TGAATTTTGT
      ThrAspTyr HisIleAsp GlnValSerAsn LeuValGlu CysLeuSer AspGluPheCys

1981  CTGGATGAAA AAAAAGAATT GTCCGAGAAA GTCAAACATG CGAAGCGACT TAGTGATGAG
      LeuAspGlu LysLysGlu LeuSerGluLys ValLysHis AlaLysArg LeuSerAspGlu
```

EP 0 645 456 A2

Fig. 15C

```
2041  CGGAATTTAC TTCAAGATCC AAACTTTAGA GGGATCAATA GACAACTAGA CCGTGGCTGG
      ArgAsnLeu LeuGlnAsp ProAsnPheArg GlyIleAsn ArgGlnLeu AspArgGlyTrp

2101  AGAGGAAGTA CGGATATTAC CATCCAAGGA GGCGATGACG TATTCAAAGA GAATTACGTT
      ArgGlySer ThrAspIle ThrIleGlnGly GlyAspAsp ValPheLys GluAsnTyrVal

2161  ACGCTATTGG GTACCTTTGA TGAGTGCTAT CCAACGTATT TATATCAAAA AATAGATGAG
      ThrLeuLeu GlyThrPhe AspGluCysTyr ProThrTyr LeuTyrGln LysIleAspGlu

2221  TCGAAATTAA AAGCCTATAC CCGTTACCAA TTAAGAGGGT ATATCGAAGA TAGTCAAGAC
      SerLysLeu LysAlaTyr ThrArgTyrGln LeuArgGly TyrIleGlu AspSerGlnAsp

2281  TTAGAAATCT ATTTAATTCG CTACAATGCC AAACACGAAA CAGTAAATGT GCCAGGTACG
      LeuGluIle TyrLeuIle ArgTyrAsnAla LysHisGlu ThrValAsn ValProGlyThr

2341  GGTTCCTTAT GGCCGCTTTC AGCCCCAAGT CCAATCGGCA AGTGCGGGGA GCCGAATCGA
      GlySerLeu TrpProLeu SerAlaProSer ProIleGly LysCysGly GluProAsnArg

2401  TGCGCTCCGC ACCTGGAGTG GAACCCGGAC CTAGACTGCA GCTGCAGGGA CGGGGAGAAG
      CysAlaPro HisLeuGlu TrpAsnProAsp LeuAspCys SerCysArg AspGlyGluLys

2461  TGCGCCCACC ACAGCCACCA CTTCAGCCTG GACATCGACG TGGGCTGCAC CGACCTGAAC
      CysAlaHis HisSerHis HisPheSerLeu AspIleAsp ValGlyCys ThrAspLeuAsn

2521  GAGGACCTGG GCGTGTGGGT GATCTTCAAG ATCAAGACCC AGGACGGCCA CGCCCGCCTG
      GluAspLeu GlyValTrp ValIlePheLys IleLysThr GlnAspGly HisAlaArgLeu

2581  GGCAATCTAG AATTTCTCGA AGAGAAACCA TTAGTAGGAG AAGCACTAGC TCGTGTGAAA
      GlyAsnLeu GluPheLeu GluGluLysPro LeuValGly GluAlaLeu AlaArgValLys

2641  AGAGCGGAGA AAAAATGGAG AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATTGTT
      ArgAlaGlu LysLysTrp ArgAspLysArg GluLysLeu GluTrpGlu ThrAsnIleVal

2701  TATAAAGAGG CAAAAGAATC TGTAGATGCT TTATTTGTAA ACTCTCAATA TGATAGATTA
      TyrLysGlu AlaLysGlu SerValAspAla LeuPheVal AsnSerGln TyrAspArgLeu

2761  CAAGCGGATA CCAACATCGC GATGATTCAT GCGGCAGATA AACGCGTTCA TAGCATTCGA
      GlnAlaAsp ThrAsnIle AlaMetIleHis AlaAlaAsp LysArgVal HisSerIleArg

2821  GAAGCTTATC TGCCTGAGCT GTCTGTGATT CCGGGTGTCA ATGCGGCTAT TTTTGAAGAA
      GluAlaTyr LeuProGlu LeuSerValIle ProGlyVal AsnAlaAla IlePheGluGlu

2881  TTAGAAGGGC GTATTTTCAC TGCATTCTCC CTATATGATG CGAGAAATGT CATTAAAAAT
      LeuGluGly ArgIlePhe ThrAlaPheSer LeuTyrAsp AlaArgAsn ValIleLysAsn

2941  GGTGATTTTA ATAATGGCTT ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA
      GlyAspPhe AsnAsnGly LeuSerCysTrp AsnValLys GlyHisVal AspValGluGlu

3001  CAAAACAACC ACCGTTCGGT CCTTGTTGTT CCGGAATGGG AAGCAGAAGT GTCACAAGAA
      GlnAsnAsn HisArgSer ValLeuValVal ProGluTrp GluAlaGlu ValSerGlnGlu
```

5,965,742

Fig. 15D

5,968,745 - 4/5/2001

```
3061  GTTCGTGTCT GTCCGGGTCG TGGCTATATC CTTCGTGTCA CAGCGTACAA GGAGGGATAT
      ValArgVal CysProGly ArgGlyTyrIle LeuArgVal ThrAlaTyr LysGluGlyTyr

3121  GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAATA CAGACGAACT GAAGTTTAGC
      GlyGluGly CysValThr IleHisGluIle GluAsnAsn ThrAspGlu LeuLysPheSer

3181  AACTGTGTAG AAGAGGAAGT ATATCCAAAC AACACGGTAA CGTGTAATGA TTATACTGCG
      AsnCysVal GluGluGlu ValTyrProAsn AsnThrVal ThrCysAsn AspTyrThrAla

3241  ACTCAAGAAG AATATGAGGG TACGTACACT TCTCGTAATC GAGGATATGA CGGAGCCTAT
      ThrGlnGlu GluTyrGlu GlyThrTyrThr SerArgAsn ArgGlyTyr AspGlyAlaTyr

3301  GAAAGCAATT CTTCTGTACC AGCTGATTAT GCATCAGCCT ATGAAGAAAA AGCATATACA
      GluSerAsn SerSerVal ProAlaAspTyr AlaSerAla TyrGluGlu LysAlaTyrThr

3361  GATGGACGAA GAGACAATCC TTGTGAATCT AACAGAGGAT ATGGGGATTA CACACCACTA
      AspGlyArg ArgAspAsn ProCysGluSer AsnArgGly TyrGlyAsp TyrThrProLeu

3421  CCAGCTGGCT ATGTGACAAA AGAATTAGAG TACTTCCCAG AAACCGATAA GGTATGGATT
      ProAlaGly TyrValThr LysGluLeuGlu TyrPhePro GluThrAsp LysValTrpIle

3481  GAGATCGGAG AAACGGAAGG AACATTCATC GTGGACAGCG TGGAATTACT TCTTATGGAG
      GluIleGly GluThrGlu GlyThrPheIle ValAspSer ValGluLeu LeuLeuMetGlu

3541  GAATAAG
      Glu---
```

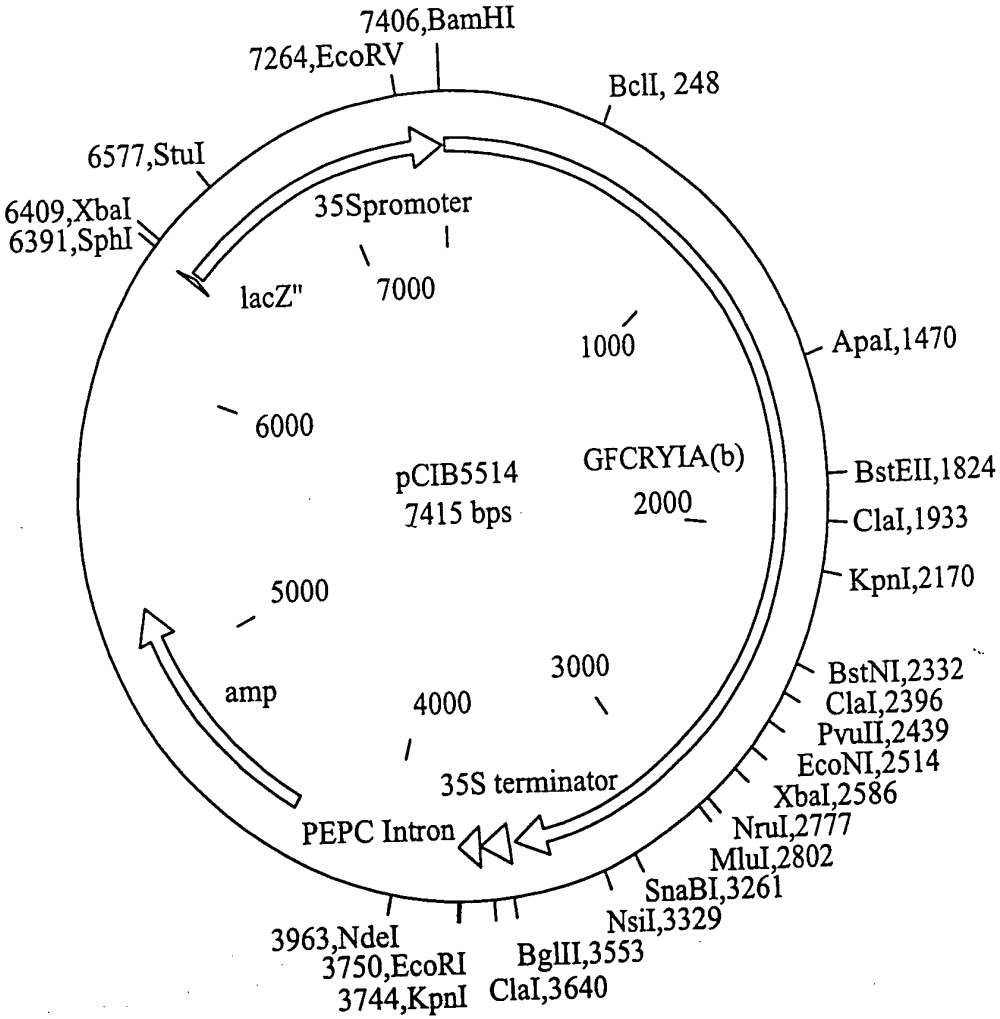

7406,BamHI
7264,EcoRV
BclI, 248
6577,StuI
6409,XbaI
6391,SphI
35Spromoter
lacZ"
7000
1000
ApaI,1470
6000
pCIB5514
7415 bps
GFCRYIA(b)
2000
BstEII,1824
ClaI,1933
KpnI,2170
5000
3000
BstNI,2332
ClaI,2396
PvuII,2439
amp
4000
EcoNI,2514
XbaI,2586
35S terminator
NruI,2777
PEPC Intron
MluI,2802
SnaBI,3261
NsiI,3329
3963,NdeI
3750,EcoRI
3744,KpnI
BglII,3553
ClaI,3640

Fig. 16

TOOZTT" 29h88660

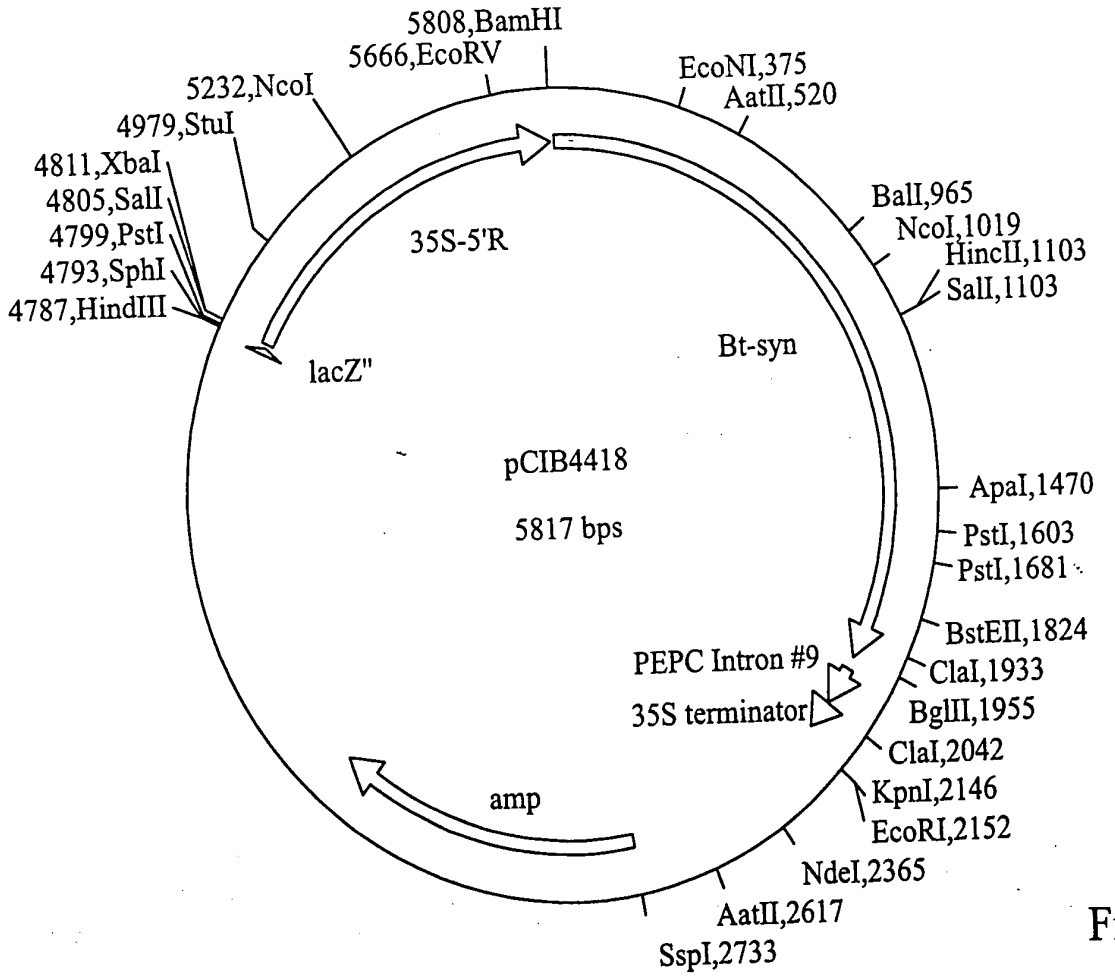


Fig. 17

FOREIGN 29438660

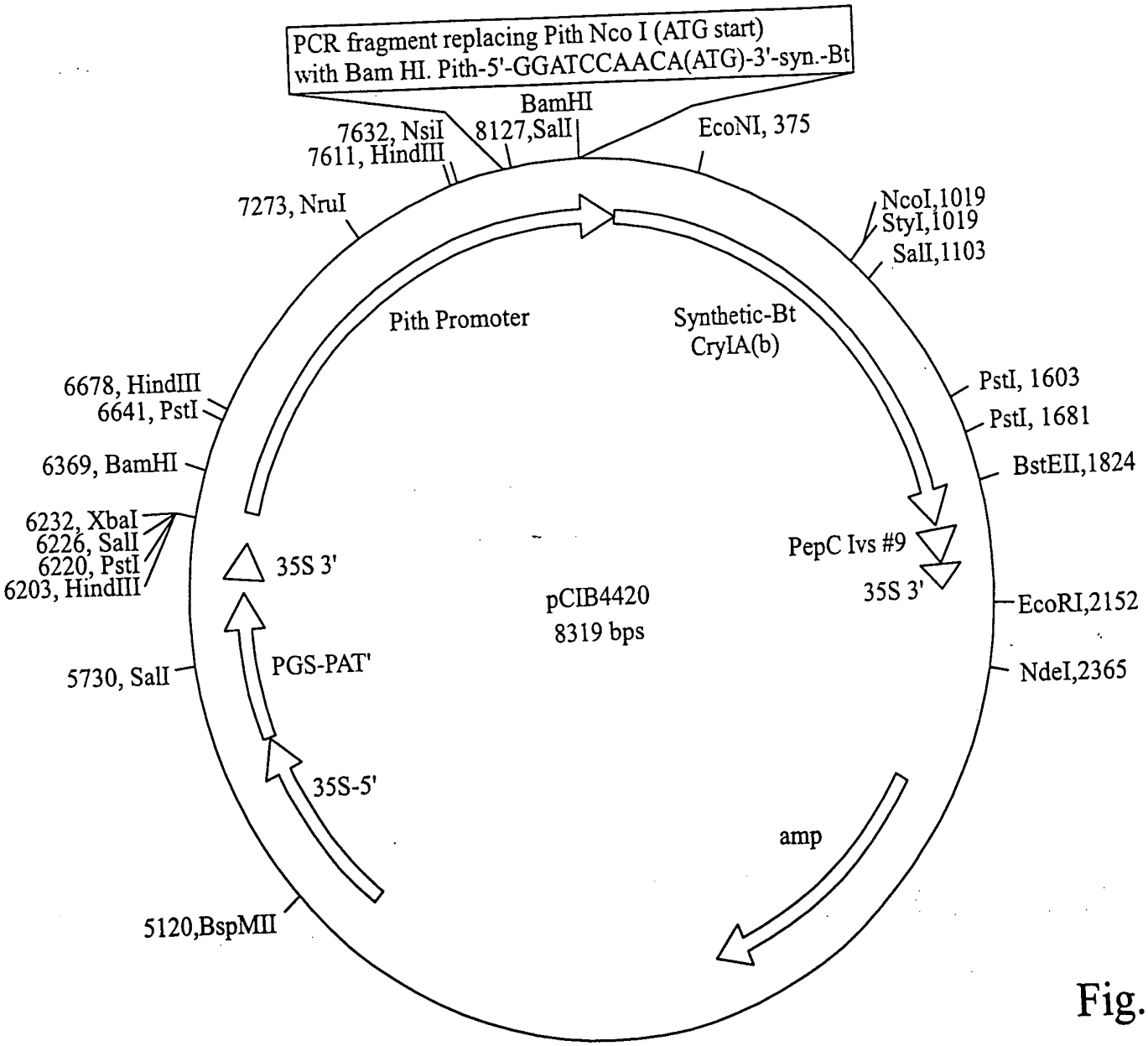


Fig. 18

T0027T" 29h8860

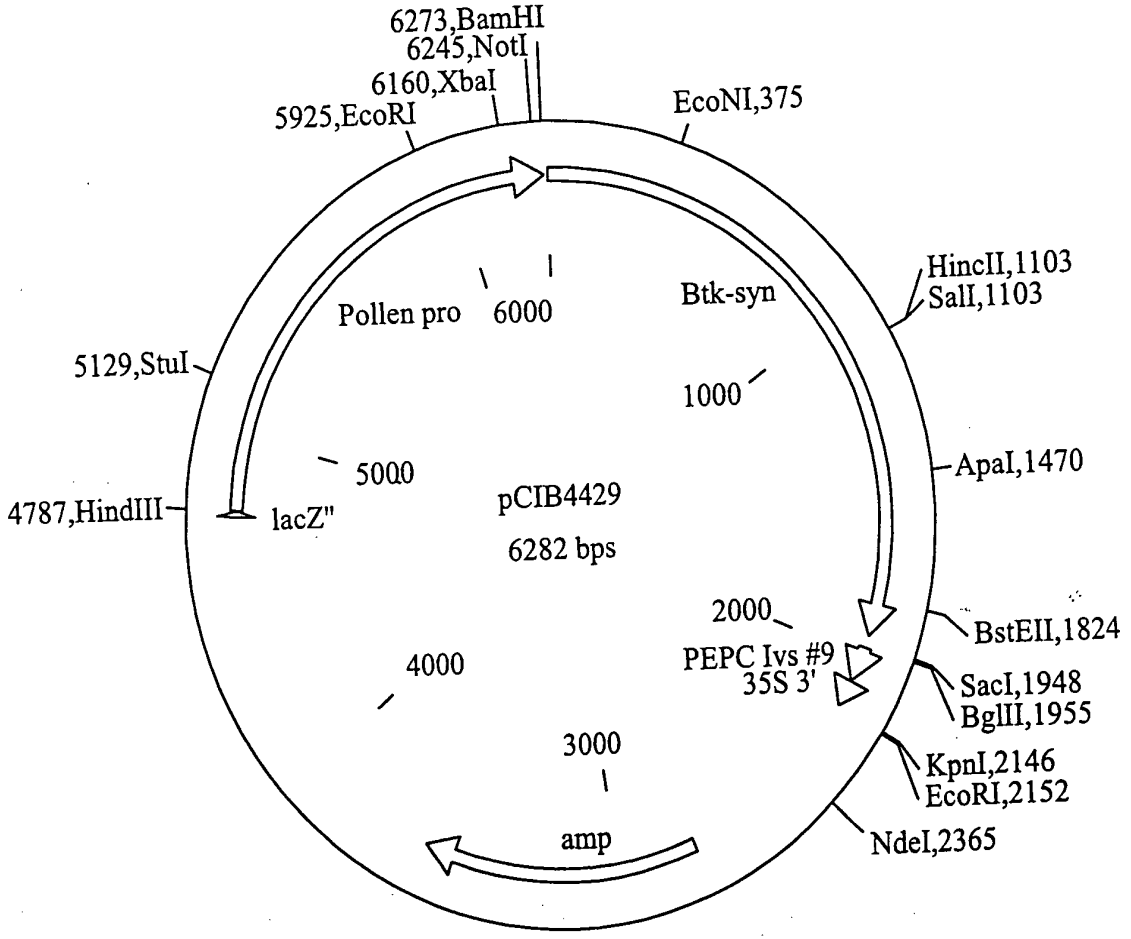


FIG. 19

T002TT" 29h88660

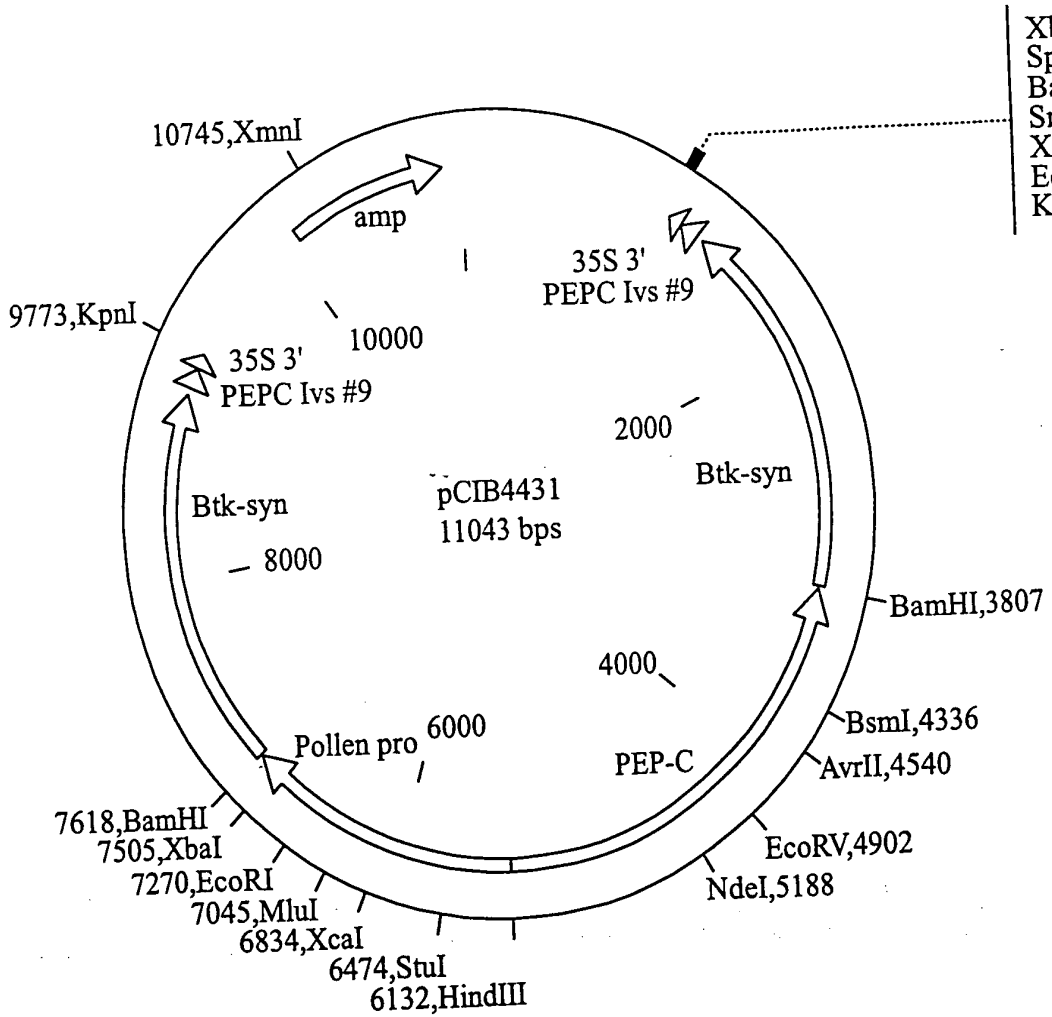


FIG. 20

T002TT" 29h88660

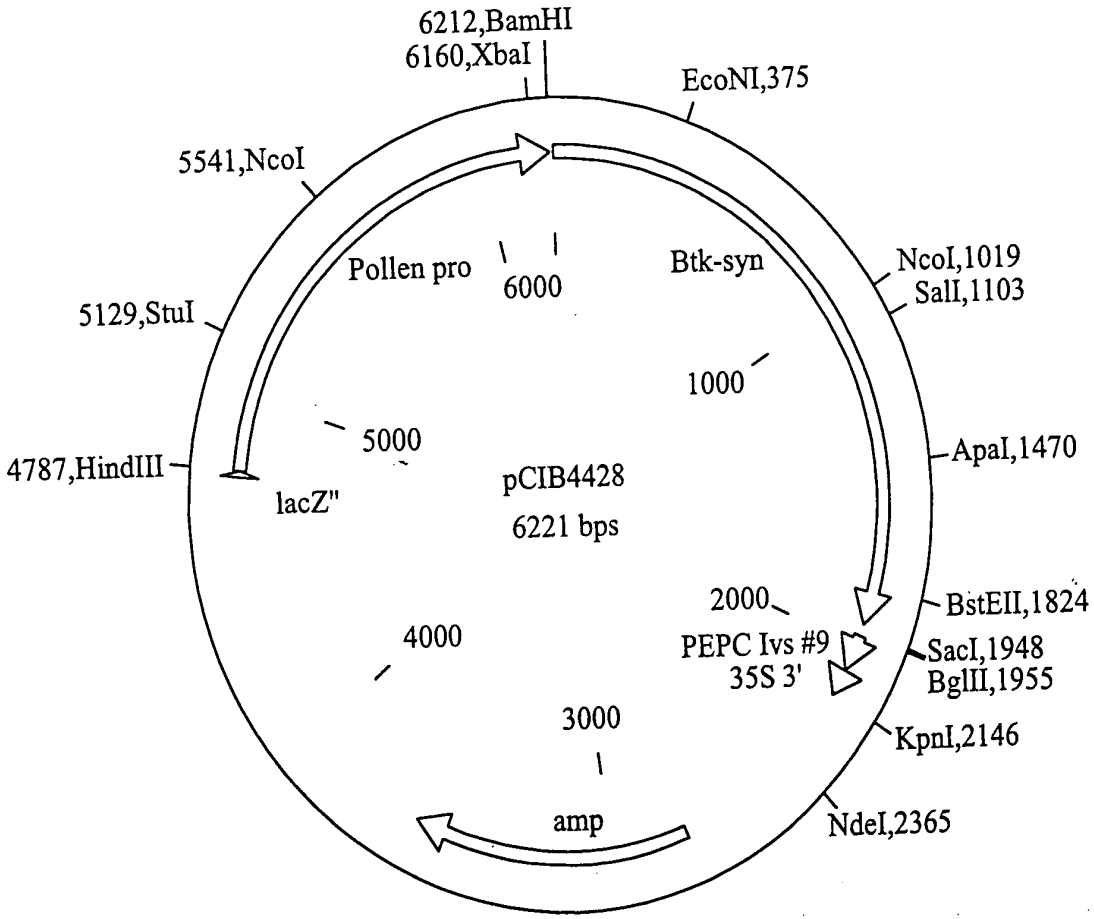


FIG. 21

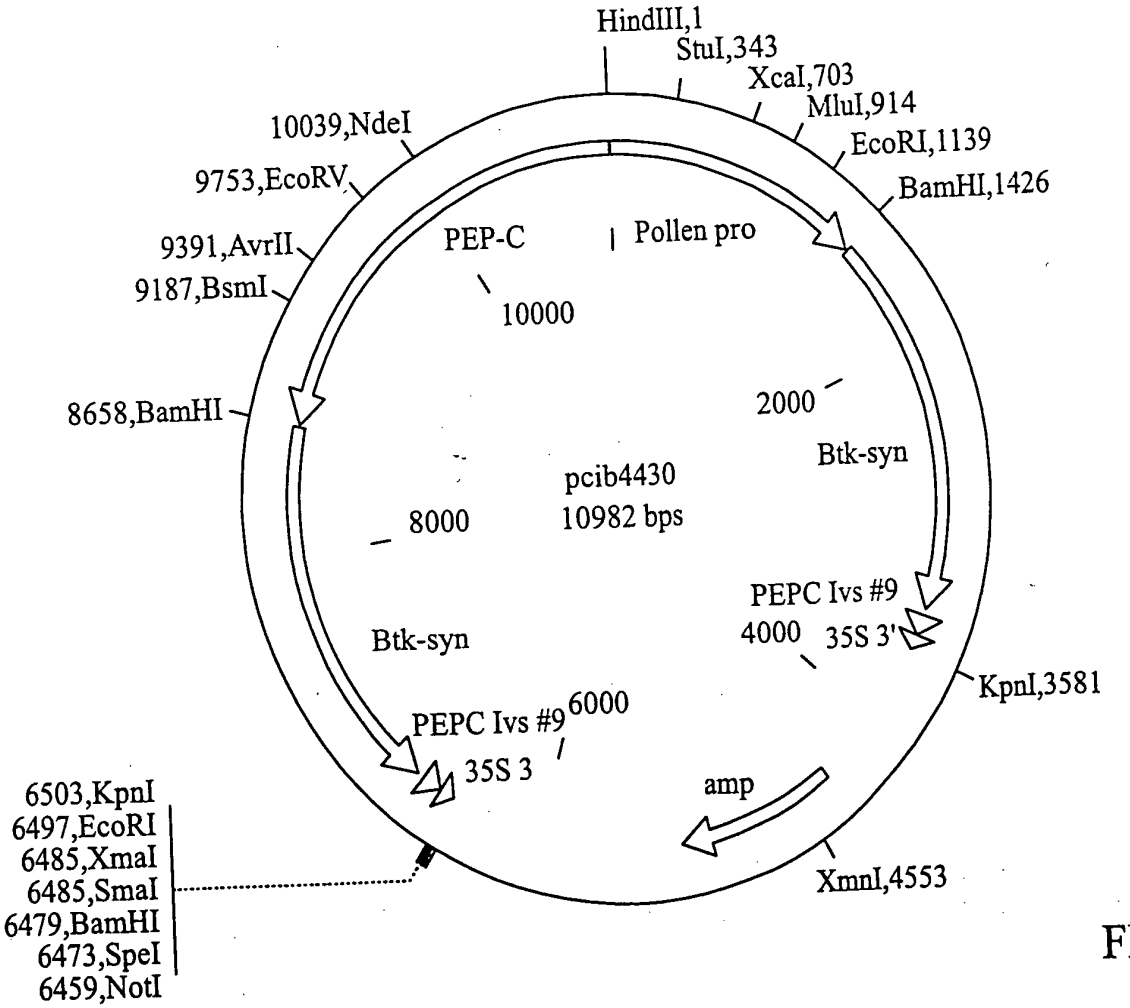

HindIII,1
StuI,343
XcaI,703
MluI,914
EcoRI,1139
BamHI,1426
10039,NdeI
9753,EcoRV
9391,AvrII
9187,BsmI
8658,BamHI
PEP-C
Pollen pro
10000
2000
Btk-syn
pcib4430
10982 bps
8000
PEPC Ivs #9
4000
35S 3'
KpnI,3581
Btk-syn
PEPC Ivs #9
6000
35S 3
amp
XmnI,4553
6503,KpnI
6497,EcoRI
6485,XmaI
6485,SmaI
6479,BamHI
6473,SpeI
6459,NotI

FIG. 22

Fig. 23A

CrylA(b) Protein Levels in Transgenic Maize

ELISA Bt Values of Field Plants:

INBRED X PARENT	ABRU PLANT Number	ng Bt/mg protein
2ND01X171-4A	1646	29
5N984X171-4A	857	1705
5N984X171-4A	870	1760
5N984X171-13	969	22
5N984X171-15	1468	17
5N984X171-15	1470	28
5N984X171-14A	1502	180
5N984X171-14A	1529	1500
5N984X176-11	1667	408
5N984X176-11	1671	1270
5N984X176-11	1673	1522
5N984X176-11	1675	943
5N984X176-11	1679	967
5N984X171-4B	1942	15
5N984X171-4B	1946	16
5NA56X171-16ABX	1101	30
5NA89X176-11	1622	959
5NA89X176-11	1630	1172
5NA89X176-11	1635	1100
6F010X171-4	825	103
6F010X171-4	832	1298

-Bt levels are in ng crylA(b)/mg total protein.

-Data are from progeny of the described maize transformants expressing the crylA(b) protein.

-ELISA analysis of transgenic plant material was carried out using standard procedures as described elsewhere.

EP 0 385 962 B1

T002TT"29h88660

Fig. 23B

Bioassay of European corn borer, Ostrinia nubilalis, and sugarcane borer, Diatraea saccharalis

Plasmid	Promoter	Cross	Plant No.	Bt Gene	Percent Mortality	
					Ostrinia	Diatraea
pCIB4431	PEPC	5N984 X 176-8B	21	+	100	100
			22	-	0	0
			40	+	100	100
pCIB4431	PEPC	5N984 X 176-11	95	+	100	100
			96	-	0	0
			98	+	100	100
pCIB4418	35S	5N984 X 171-14A	45	-	0	10
			64	+	100	90
			68	+	100	100
pCIB4431	PEPC	2N217AF X 176-8B	1	-	0	0
			3	+	100	100
			4	+	100	100
pCIB4418	35S	2N217AF X 171-15	70	-	10	0
			83	+	90	80
			88	+	90	100

Fig. 23C

CrylA(b) Protein Levels in Transgenic Maize

Greenhouse plants

35S LINE	LEAF	PITH	ROOT	POLLEN
6F010 x 171-4A	-409 + 288	NT	NT	NT
5N984 x 171-14A	256 + 159	191	198	30
6F010 x 171-16AB	240 + 174	221	271	NT
5N984 x 171-13	201 + 94	NT	NT	NT
5NA89 x 171-13	37 + 7	150	0	NT
5N984 x 171-18	7.7 + 3	NT	NT	NT
6N615 x 171-16AB	7.5 + 3	0	0	
PEPC LINE				
6N615 x 176-11	1126 + 419	41	19	NT
6F010 x 176-10	774 + 159	NT	NT	130
5N984 x 176-11	719 + 128	16	20	186

-Bt levels are in ng crylA(b)/mg total protein.

Data are from progeny of the described maize transformants expressing the crylA(b) protein.

ELISA analysis of transgenic plant material was carried out using standard procedures as described elsewhere.

T0021-9804-0

T0027T "29h88660

Fig. 23D

Bioassay of European corn borer, Ostrinia nubilalis, on Pith:SynBt maize

Plasmid	Promoter	Event	Plant No.	Percent Mortality
pCIB4433	Pith	JS21A-Top	1	90
			3	80
			11	90
			13	70
			14	75
			19	85
			28	80
pCIB4433	Pith	JS22D-Mid	3	70
			4	65
			7	85
			17	95
		Control	1	5
			2	0
			3	0

Fig. 23E

EXPRESSION OF THE CRYIA(b) GENE IN TRANSGENIC MAIZE USING THE PITH-PREFERRED PROMOTER

Leaf samples from small plantlets transformed with pCIB4433 using procedures described elsewhere were analyzed for the presence of the crylA(b) protein using ELISA. All plants expressing crylA(b) were found to be insecticidal in the standard European corn borer bioassay.

Note that the pith-preferred promoter has a low, but detectable level of expression in leaf tissue of maize. Detection of CrylA(b) protein is consistent with this pattern of expression.

PLANT NUMBER	ng crylA(b)/mg protein
JS21A-1 TOP	169
JS21A-2 TOP	0
JS21A-3 TOP	113
JS21A-11 TOP	127
JS21A-12 TOP	112
JS21A-13 TOP	97
JS21A-14 TOP	118
JS21A-19 TOP	82
JS21A-24 TOP	0
JS21A-28 TOP	154
JS22D-3 MID	2946
JS22D-4 MID	5590
JS22D-11 MID	215
JS22D-17 MID	3004

960450 - 112004

Fig. 24A

```
  1 GAATTCGGATCCATTAAAGAAGTCTTTGAACAGATTCTAGAGATCTAGTTTAATGAGCTC  60
 61 CCAAAAGTCTTGAAAAAATTCAGCGGGGAGGCCATTAGGGCAGGGGTACTGTTATGTTTT 120
121 AAAGAGAACACCACTTTCTTGATCTCTTCTAAAGAGAAATGTTTTGTAAGAAGGATCCTG 180
181 TCCTCCTCATCCAACCTTTTCATCGGCAAATTTTTCATAGAGATATTAGAGGCAAGAGAG 240
241 GGGCCAAAAAGATCCATGTAAATGGAAGTGGCCACCTGGTTGATACCTCCCTCATCTTCA 300
301 ACAGAAAATCCATTATGAAAAAGTGAATGGATTTTAAACTCTTCTTTTTCTTCCCTTTTG 360
361 CAATGAGCTGAAAATATCTGGTATTATTCTCATCACCCTCATTAATGAATCTGTCCCTAG 420
421 CAATTTGCTTTCTCTTGATCCCTTCTGCAGCCACCATGTTTCTTAAATTCCACTCCATAT 480
481 CAAGCTTTTCCAATCTATCAGAATCTGAGATGGCTGCAATCTCTCTCATTTTCTCAAGGA 540
541 TATCGATGTTATCCATAAGGTATTTCTTGAACTTCTTATATTTCCCTTCGACATTTATAT 600
601 TCCATCCTTTCAACATTTTTTTGTTCAATCTTTTTTGTTTTTTTCCTTTCCAAACATCGA 660
661 TACATTTCCTGCTCCTCACAGGTAAGGACGAGCTTTCAAAAAACCTTCTGCTTTAAAGTC 720
721 AGGTCTGAGCCTCCAGCAAAGCTCACATATCTAAAGTCCCTCTTCTTAGTTGGGACAGAG 780
781 TCAGTGCTAAGACACATGGGAACATGACCAGAAAAAAAAAAATCATATTTAGCCCAGAGAC 840
841 AACAATATTCTTGTACTGCAAGTCTCGTTATGGGCTAGCAAAGGAATCTACCCAACTTCT 900
901 CAAATGTGTTGGGATGTCAAGTATATAGACTATTCATCAGTTCCAACTCTATCAAACTGT 960
961 GCAGCTCAATTATAGAGTTGAATAAAGTGCTCCATCTATTTGTTCTTATCCTCATATTTG 1020
1021 GTTAAGATATTAAAATCACCTCCCACCAACATTTAAAGTGCACCATTTAAAGTGGCTCGC 1080
1081 GAGCACCAAACCGCTGAAAACCGGAAATGTTTAGCACGTTGGCAGCGGGACCCTTTTCTA 1140
1141 TCTCATCGTGTTCTTCGTTGTCCACCACGGCCCACGGGCCAACGCTCCTCCATCCTGTAG 1200
1201 TGTAGAGTATATTCCATTTGCGACCGAGCCGAGCATCGATCCAGCCACACTGGCCACTGC 1260
                                                  84
1261 CAGCCAGCCATGTGGCACTCCTACGTATACTACGTGAGGTGAGATTCACTCACATQGGAT 1320
-465                                                              -405

1321 GGGACCGAGATATTTTACTGCTGTGGTTGTGTGAGAGATAATAAAGCATTTATGACGATT 1380
1381 GCTGAACAGCACACACCATGCGTCCAGATAGAGAAAGCTTTCTCTCTTTATTCGCATGCA 1440

1441 TGTTTCATTATCTTTTATCATATATATATAACACATATTAAATGATTCTTCGTTCCAATT 1500
-285                                                              -226

1501 TATAATTCATTTGACTTTTTTATCCACCGATGCTCGTTTTATTAAAAAAAATATTATAAT 1560
-225                                                              -166

1561 TATTGTTACTTTTTGTTGTAATATTGTTTAGCATATAATAAACTTTGATACTAGTATGTT 1620
-165                                                              -106
                                              49
1621 TCCGAGCAAAAAAAAATATTAATATTTAGATTACGAGCCCATTAATTAATTATATTCGAG 1680
-105                                                               -46
                                  83                    +1
1681 ACAAGCGAAGCAAAGCAAAGCAAGCTAATGTTGCCCCTGCTGTGCATGCAGAGGCCCGCT 1740
-45                                                               +15
                                                          73*******
1741 CTTGCTATAAACGAGGCAGCTAGACGCGACTCGACTCATCAGCCTCATCAACCTCGACGA 1800
 +16                                                              +75
      ***************                          ▼
1801 AGGAGGAACGAACGGACAGGTTGTTGCACAGAAGCGACATGGCTTTCGCGCCCAAAACGT 1860
 +76                                          M  A  F  A  P  K  T  S +135
```


5,968,750

Fig. 24B

```
1861 CCTCCTCCTCCTCGCTGTCCTCGGCGTTGCAGGCAGCTCAGTCGCCGCCGCTGCTCCTGA 1920
+126   S  S  S  S  L  S  S  A  L  Q  A  A  Q  S  P  P  L  L  L  R +195

                                                  40 + 41
1921 GGCGGATGTCGTCGACCGCAACACCGAGACGGAGGTACGACGCGGCCGTCGTCGTCACTA 1980
+196   R  M  S  S  T  A  T  P  R  R  R  Y  D  A  A  V  V  V  T  T +255

1981 CCACCACCACTGCTAGAGCTGCGGCGGCTGCTGTCACGGTTCCCGCCGCCCCGCCGCAGG 2040
+256   T  T  T  A  R  A  A  A  A  A  V  T  V  P  A  A  P  P  Q  A +315

                                                 75                $
2041 CGGGCCGCCGCCGCCGGTGCCACCAAAGCAAGCGGCGGCACCCGCAGAGGAGGAGCCGTC 2100
+316   G  R  R  R  R  C  H  Q  S  K  R  R  H  P  Q  R  R  S  R  P +375

2101 CGGTGTCGGACACCATGGCGGCGCTCATGGCCAAGGGCAAGGTTCGTATAGTACGCGCGC 2160
+376   V  S  D  T  M  A  A  L  M  A  K  G  K

2161 GTGTCGTCGTCGTTATTTTGCGCATAGGCGCGGACATACACGTGCTTTAGCTAGCTAACA 2220
2221 GCTAGATCATCGGTGCAGACGGCGTTCATCCCGTACATCACCGCCGGCGACCCGGACCTA 2280
                     T  A  F  I  P  Y  I  T  A  G  D  P  D  L

2281 GCGACGACGGCCGAGGCGCTGCGTCTGCTGGACGGCTGTGGCGCCGACGTCATCGAGCTG 2340
     A  T  T  A  E  A  L  R  L  L  D  G  C  G  A  D  V  I  E  L

2341 GGGGTACCCTGCTCGGACCCCTACATCGACGGGCCCATCATCCAGGCGTCGGTGGCGCGG 2400
     G  V  P  C  S  D  P  Y  I  D  G  P  I  I  Q  A  S  V  A  R

2401 GCTCTGGCCAGCGGCACCACCATGGACGCCGTGCTGGAGATGCTGAGGGAGGTGACGCCG 2460
     A  L  A  S  G  T  T  M  D  A  V  L  E  M  L  R  E  V  T  P

2461 GAGCTGTCGTGCCCCGTGGTGCTCCTCTCCTACTACAAGCCCATCATGTCTCGCAGCTTG 2520
     E  L  S  C  P  V  V  L  L  S  Y  Y  K  P  I  M  S  R  S  L

2521 GCCGAGATGAAAGAGGCGGGGGTCCACGGTAACTATAGCTAGCTCTTCCGATCCCCCTTC 2580
     A  E  M  K  E  A  G  V  H

2581 AATTAATTAATTTATAGTAGTCCATTCATGTGATGATTTTTGTTTTTCTTTTTACTGACA 2640
2641 GGTCTTATAGTGCCTGATCTCCCGTACGTGGCCGCGCACTCGCTGTGGAGTGAAGCCAAG 2700
     G  L  I  V  P  D  L  P  Y  V  A  A  H  S  L  W  S  E  A  K

2701 AACAACAACCTGGAGCTGGTAGGTTGAATTAAGTTGATGCATGTGATGATTTATGTAGCT 2760
     N  N  N  L  E  L

2761 AGATCGAGCTAGCTATAATTAGGAGCATATCAGGTGCTGCTGACAACACCAGCCATACCA 2820
                                    V  L  L  T  T  P  A  I  P

2821 GAAGACAGGATGAAGGAGATCACCAAGGCTTCAGAAGGCTTCGTCTACCTGGTAGTTATA 2880
     E  D  R  M  K  E  I  T  K  A  S  E  G  F  V  Y  L

2881 TGTATATATAGATGGACGACGTAACTCATTCCAGCCCCATGCATATATGGAGGCTTCAAT 2940
2941 TCTGCAGAGACGACGAAGACCACGACGACGACTAACACTAGCTAGGGGCGTACGTTGCAG 3000

3001 GTGAGCGTGAACGGAGTGACAGGTCCTCGCGCAAACGTGAACCCACGAGTGGAGTCACTC 3060
     V  S  V  N  G  V  T  G  P  R  A  N  V  N  P  R  V  E  S  L
```

5,968,462 - 4 - 09 Oct 1999

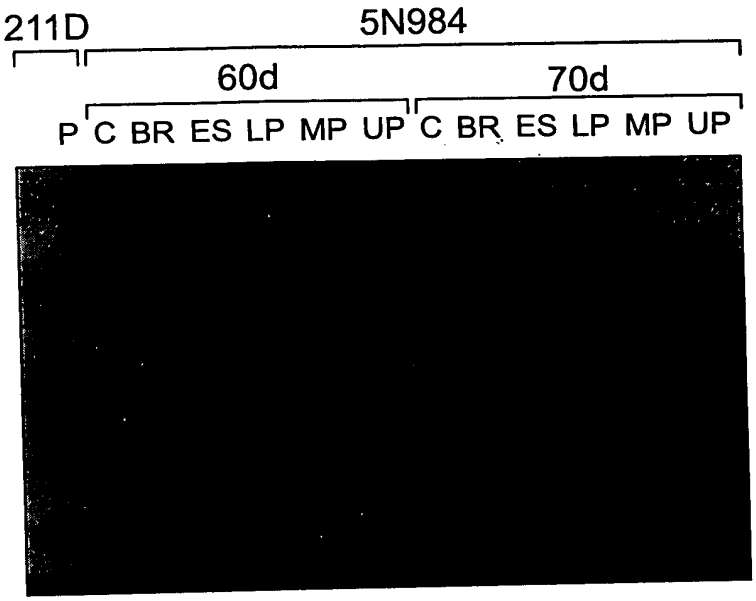
Fig. 24C

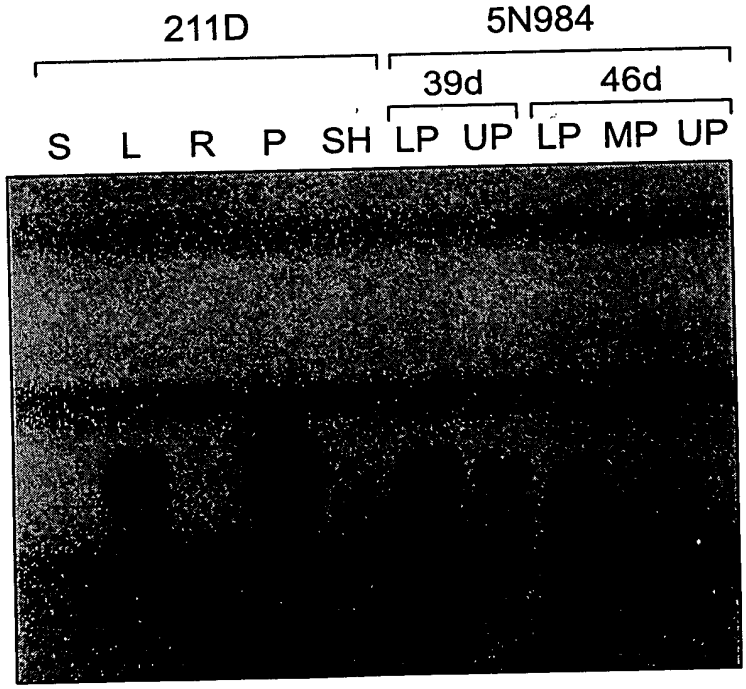
```
3061 ATCCAGGAGGTTAAGAAGGTGACTAACAAGCCCGTTGCTGTTGGCTTCGGCATATCCAAG 3120
     I  Q  E  V  K  K  V  T  N  K  P  V  A  V  G  F  G  I  S  K

3121 CCCGAGCACGTGAAGCAGGTACGTACGTAGCTGACCAAAAAAAACTGTTAACAAGTTTTG 3180
     P  E  H  V  K
3181 TTTGACAAGCCGGCTACTAGCTAGCTAACAGTGATCAGTGACACACACACACACACAGAT 3240
                                                              Q  I

3241 TGCGCAGTGGGGCGCTGACGGGGTGATCATCGGCAGCGCCATGGTGAGGCAGCTGGGCGA 3300
      A  Q  W  G  A  D  G  V  I  I  G  S  A  M  V  R  Q  L  G  E

3301 AGCGGCTTCTCCCAAGCAAGGCCTGAGGAGGCTGGAGGAGTATGCCAGGGGCATGAAGAA 3360
      A  A  S  P  K  Q  G  L  R  R  L  E  E  Y  A  R  G  M  K  N
                +++
3361 CGCGCTGCCATGAGTCCATGACAAAGTAAAACGTACAGAGACACTTGATAATATCTATCT 3420
      A  L  P
3421 ATCATCTCGGAGAAGACGACCGACCAATAAAAATAAGCCAAGTGGAAGTGAAGCTTAGCT 3480

3481 GTATATACACCGTACGTCGTCGTCGTCGTTCCGGATCGATCTCGGCCGGCTAGCTAGCAG 3540
3541 AACGTGTACGTAGTAGTATGTAATGCATGGAGTGTGGAGCTACTAGCTAGCTGGCCGTTC 3600
3601 ATTCGATTATAATTCTTCGCTCTGCTGTGGTAGCAGATGTACCTAGTCGATCTTGTACGA 3660

3661 CGAAGAAGCTGGCTAGCTAGCCGTCTCGATCGTATATGTACTGATTAATCTGCAGATTGA 3720
                                                              $

3721 ATAAAAACTACAGTACGCATATGATGCGTACGTACGTGTGTATAGTTTGTGCTCATATAT 3780
3781 GCTCCTCATCACCTGCCTGATCTGCCCATCGATCTCTCTCGTACTCCTTCCTGTTAAATG 3840
3841 CCTTCTTTGACAGACACACCACCACCAGCAGCAGTGACGCTCTGCACGCCGCCGCTTTAA 3900
3901 GACATGTAAGATATTTTAAGAGGTATAAGATACCAAGGAGCACAAATCTGGAGCACTGGG 3960
3961 ATATTGCAAAGACAAAAAAAAAAACAAAATTAAAGTCCCACCAAAGTAGAGATAGTAAAGA 4020
4021 GGTGGATGGATTAAAATTATCTCATGATTTTTGGATCTGCTCAAATAGATCGATATGGTA 4080
4081 TTCAGATCTATGTTGTATAGCCTTTTCATTAGCTTTCTGAAAAAAAAATGGTATGATGAG 4140
4141 TGCGGAGTAGCTAGGGCTGTGAAGGAGTCGGATGGGCTTCCACGTACTTGTTTGTGGCCC 4200
4201 TAGTCCGGTTCTATTTAGGTCCGATCCGAGTCCGGCATGGTCCGGTTCCATACGGGCTAG 4260
4261 GACCAAGCTCGGCACGTGAGTTTTAGGCCCGTCGGCTAGCCCGAGCACGACCCGTTTTTA 4320
4321 AACTGGCTAGGACTCGCCCATTTAATAAGACAAACATTGCAAAAAATAGCTCTATTTTTT 4380
4381 ATTTAAAATATATTGTTTATTTGTGAAATGTGTATTATTTGTAATATATATTATTGTATA 4440
4441 TAGTTATATCTTCAATTATGATTTATAAATATGTTTTTTATTATGAACTCAATTTTAAGT 4500
4501 TTGATTTATGCGTTGGCGGGCTCGAGGAGGCACGGTGAACATTTTTGGGTCGGGCTTAAC 4560
4561 GGGTCGGCCCGGCCCGGTTCGGCCCATCCACGGCCCATCCCGTGTCGGCCTCGTTCGGTG 4620
4621 AGTTCAGCCCGTCGGACAACCCGTCCCCGGCCCGGATAATTAATCGGGCCTAACCGTGGC 4680
4681 GTGCTTAAACGGTCCGTGCCTCAACGGACCGGGCCGCGGGCGGCCCGTTTGACATCTCTA 4740
4741 GTGGTGTGATTAGAGATGGCGATGGGAACCGATCACTGATTCCGTGTGGAGAATTCGATA 4800
4801 TCAAGCTTATCGATACC                                            4817
```

Entire sequence of the maize TrpA gene, with introns and exons, transcription and translation strats, start and stop of cDNA.
$ = start and end of cDNA; +1 = transcription start; 73******* = primer extension primer; ▼ = start of translation; +++ = stop codon; _____ = CCAAT Box, TATAA Box, poly A addition site.
# above underlined sequences are PCR primers.

EP 0 462 065 B1

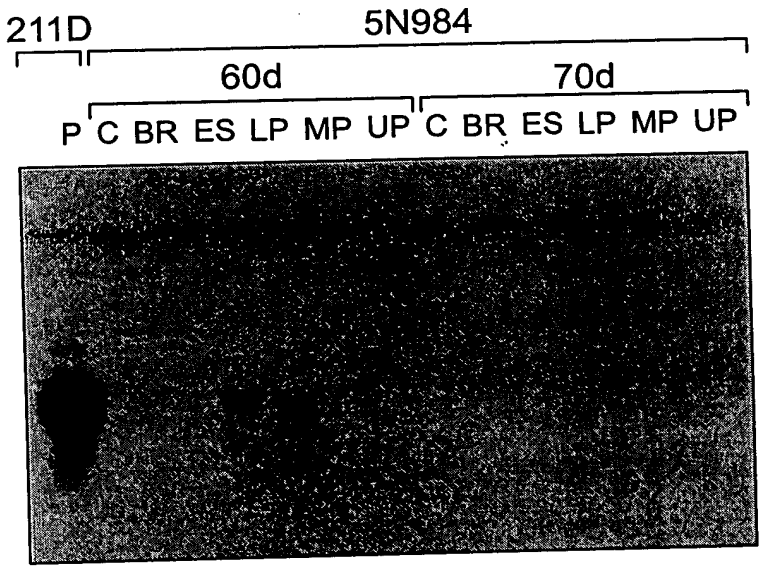
PCT/US2004/009669

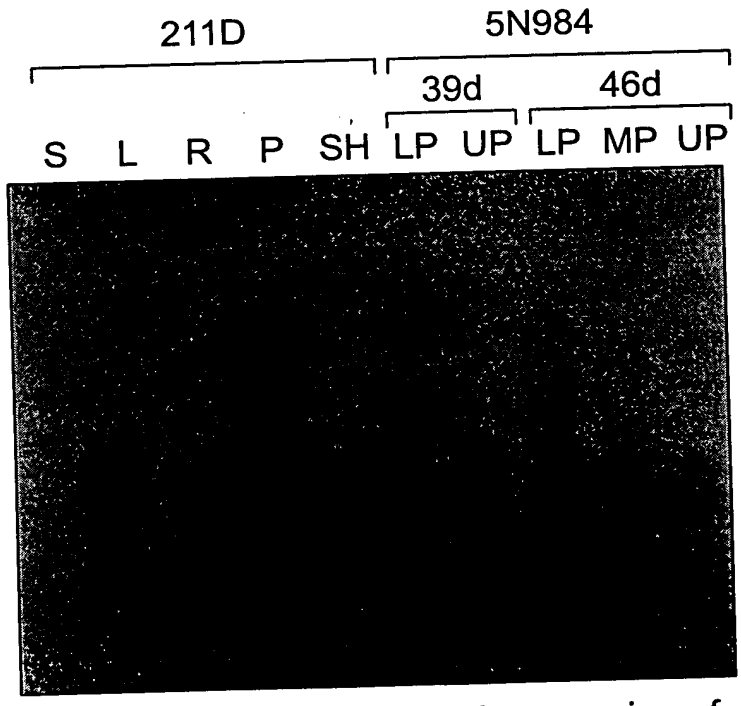




Northern blot showing differential expression of TrpA gene in maize tissues. 2 hour exposure against film at -80C with Dupont Cronex intensifying screens.

Fig. 25A

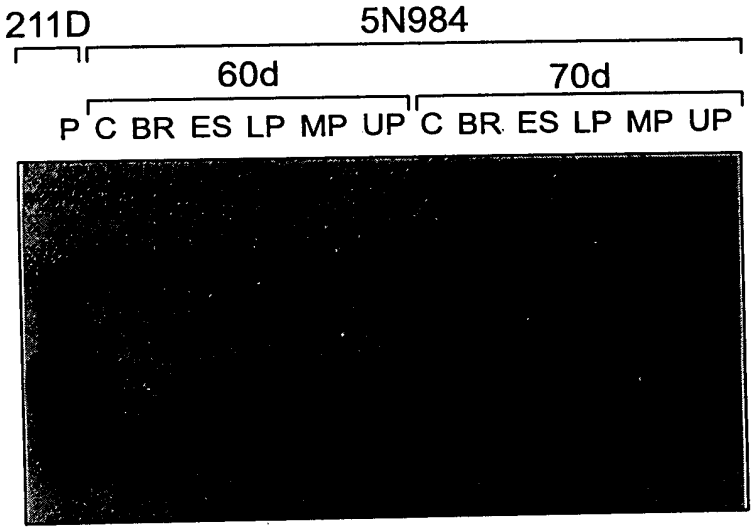


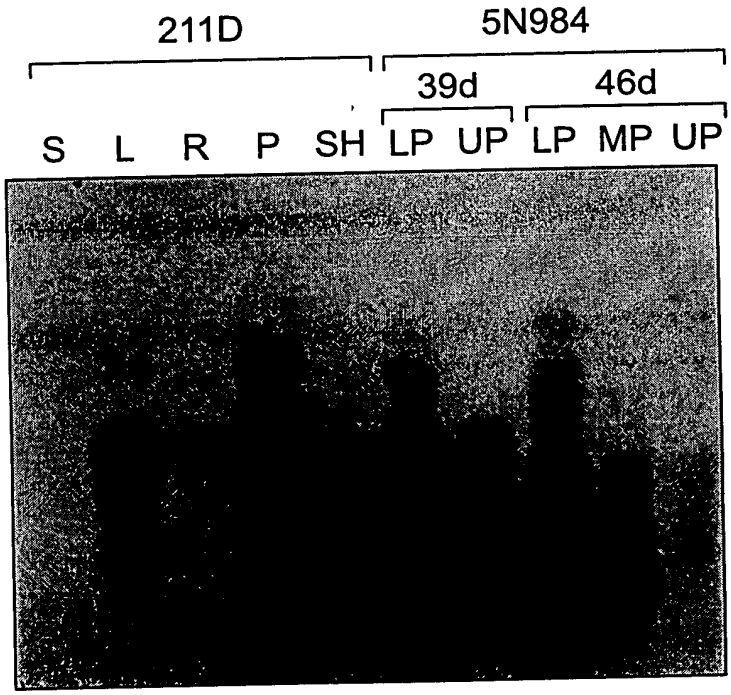


Northern blot showing differential expression of TrpA gene in maize tissues. 4 hour exposure against film at -80C with Dupont Cronex intensifying screens.

Fig. 25B

Docket: 5956-2

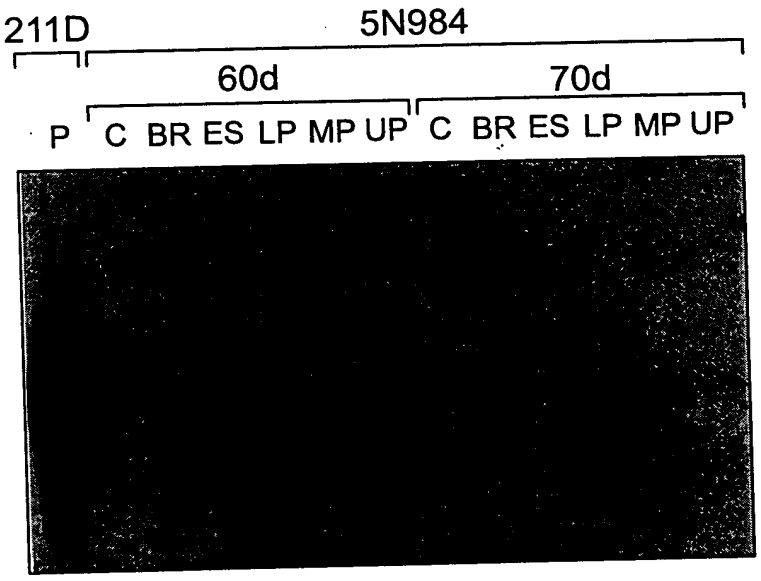


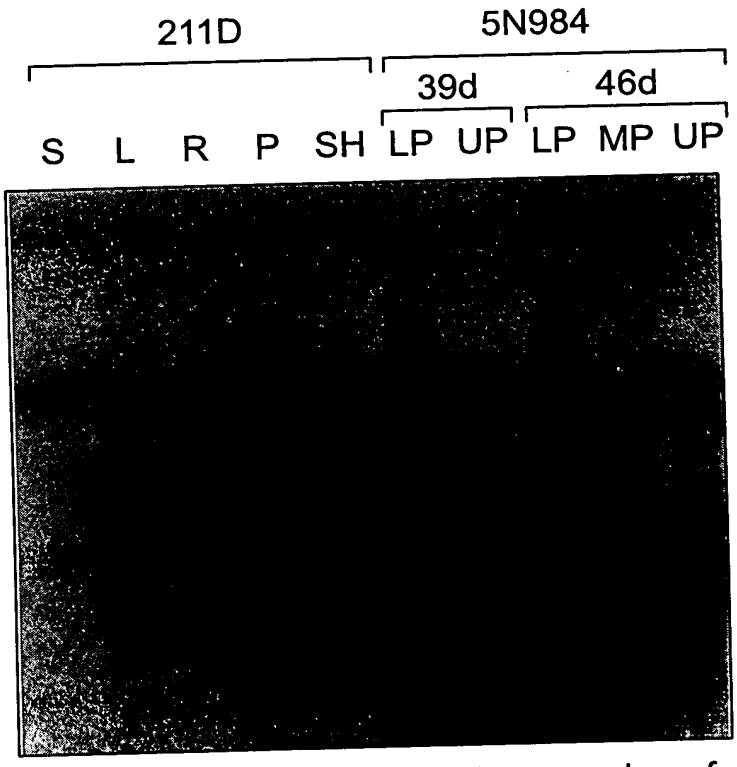


Northern blot showing differential expression of TrpA gene in maize tissues. 18 hour exposure against film at -80C with Dupont Cronex intensifying screens.

Fig. 25C

09984462 - 112204



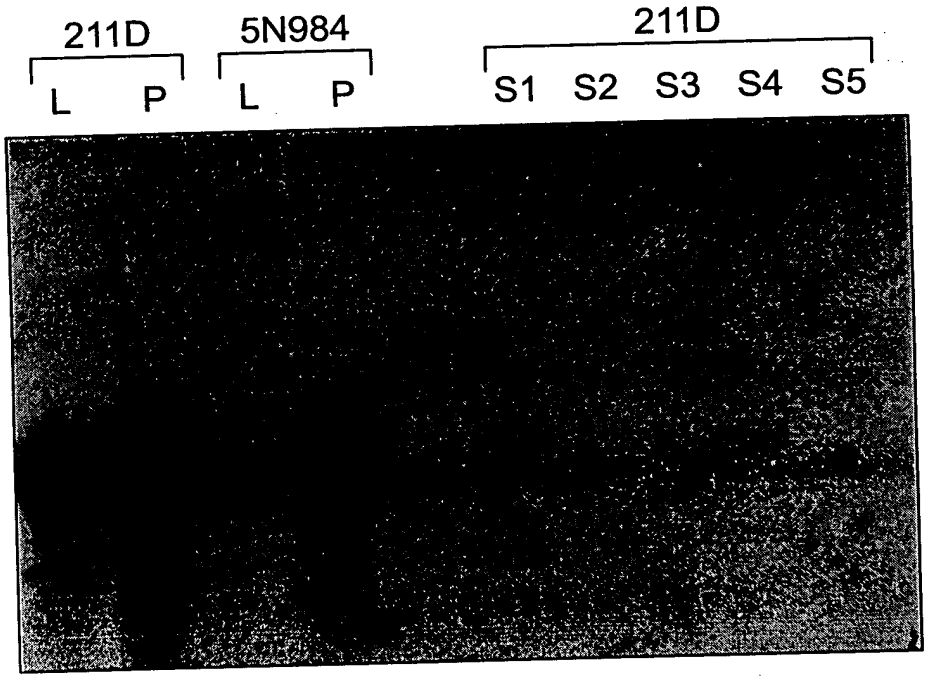


Northern blot showing differential expression of TrpA gene in maize tissues. 48 hour exposure against film at -80C with Dupont Cronex intensifying screens.

Fig. 25D

Patent: 5,959,091

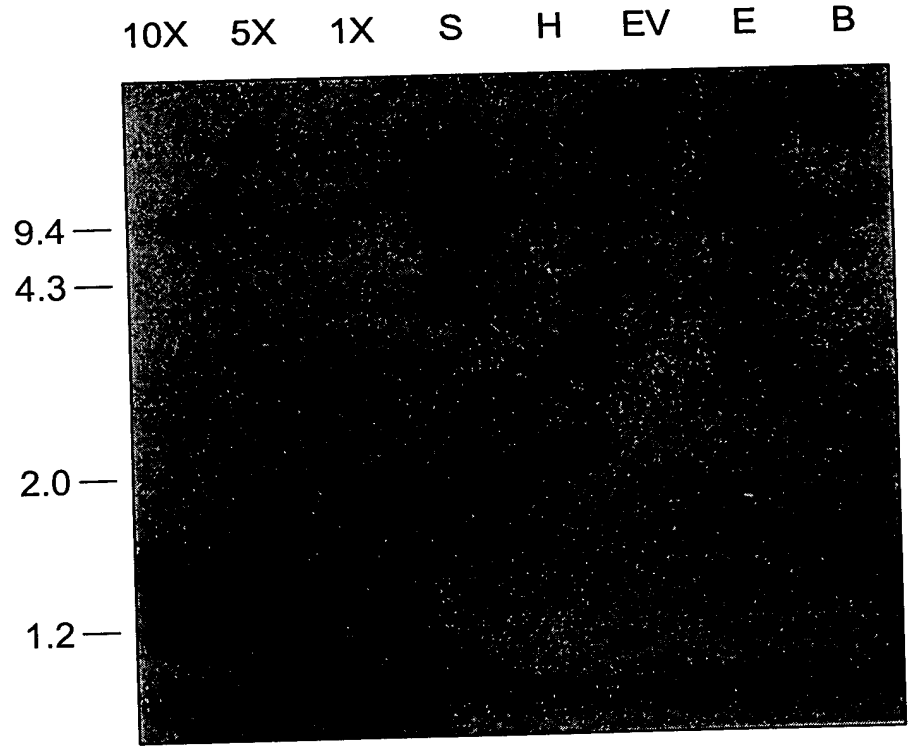
Docket - 26462-1200



Northern blot showing maize TrpA gene expression in Funk lines 211D and 5N984 leaf and pith and the absense of expression in 211D seed total RNA.
65 hour exposure against film at -80C with Dupont Cronex intensifying screens.

Fig. 26

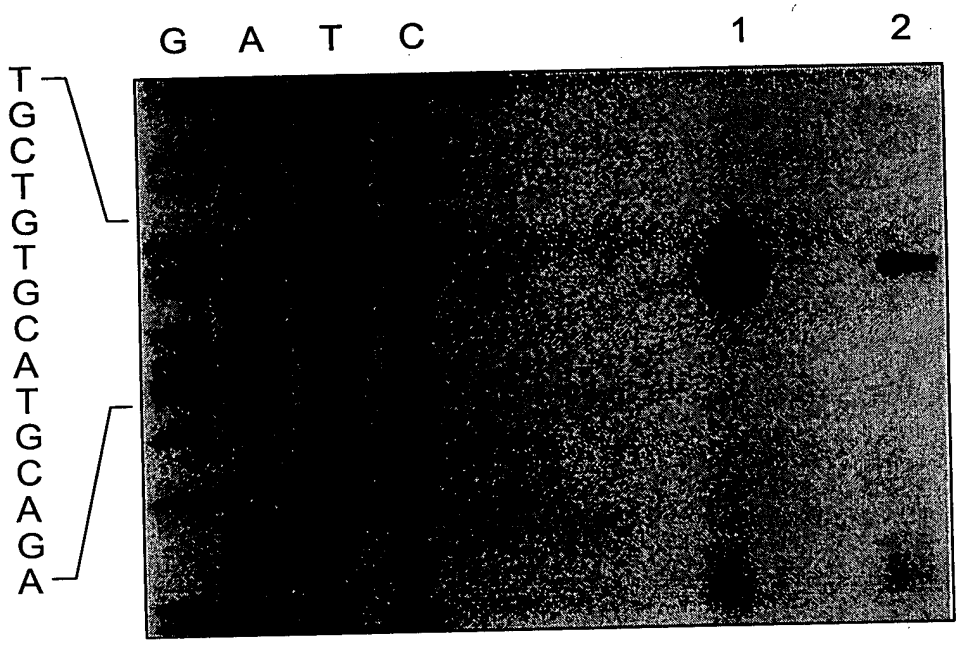
09884462 - 112201



Genomic southern of Funk line 211D probed with the TrpA cDNA 8-2. B = BamHI, E = EcoRI, EV = EcoRV, H = HindIII and S = SacI.
120 hour exposure against film at -80C with Dupont Cronex intensifying screens.

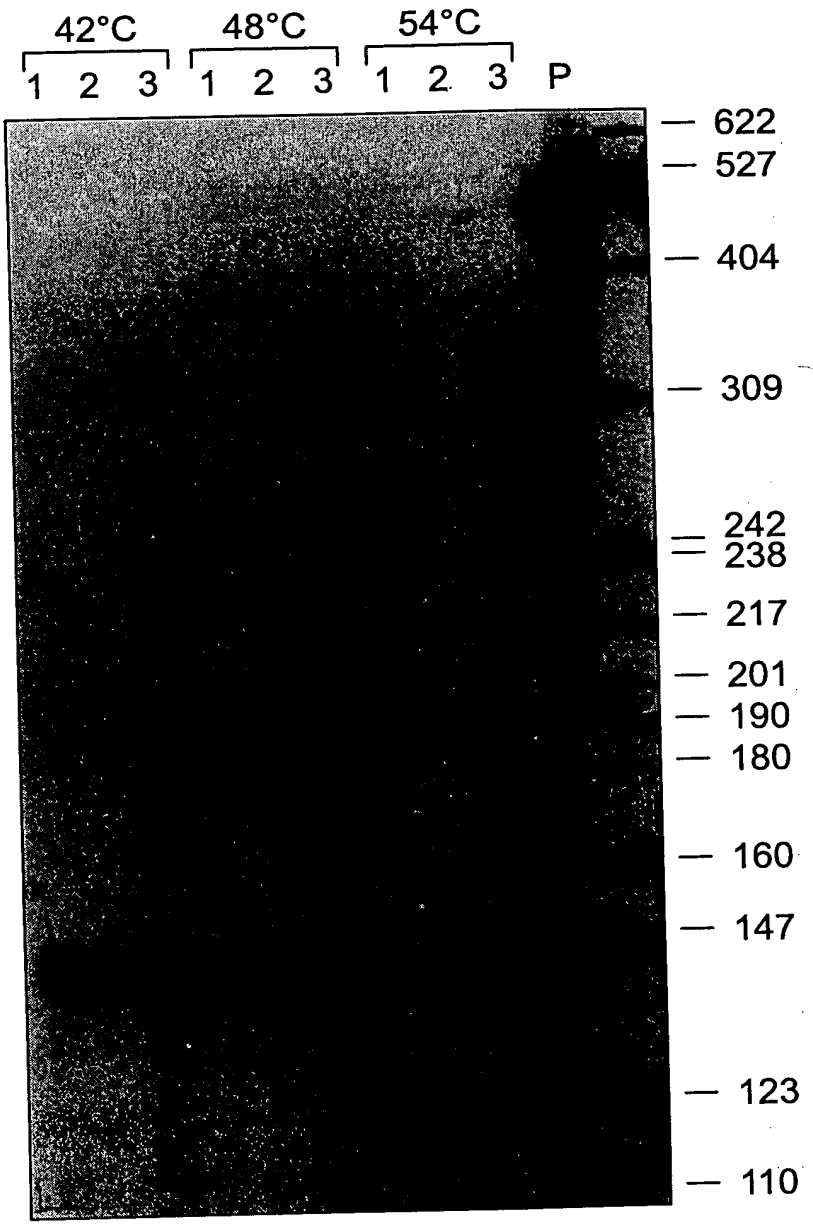
Fig. 27

09984452 - 112004



Primer extension showing the transcription start of TrpA gene and sequencing ladder.
1 hour exposure against film at -80C with Dupont Cronex intensifying screens.

Fig. 28A

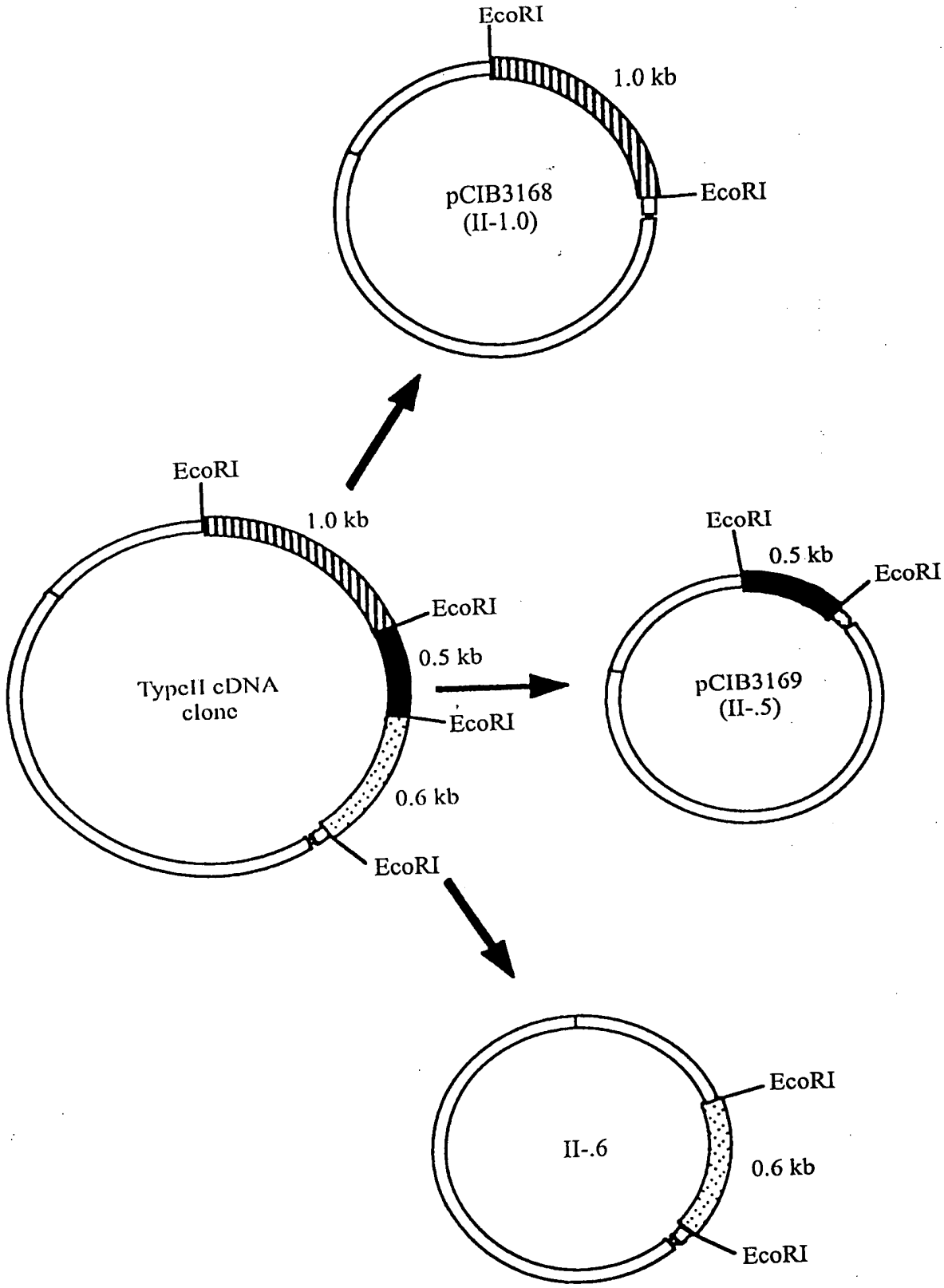


RNase protection of region from +2 bp to +387 bp
with three annealing temperatures.
16 hour exposure against film at -80C with Dupont Cronex
intensifying screens.

Fig. 28B

0568452 - 47203

Fig. 29



Patent - 5,268,463

Fig. 30B

```
969 CTG GAT AGA GAA GAG CAC CTT TAC ACA GCA TTC CAG TAT TTC GAC AAG GAC AAC AGC
323▶Leu Asp Arg Glu Glu His Leu Tyr Thr Ala Phe Gln Tyr Phe Asp Lys Asp Asn Ser

1026 GGG TAC ATT ACT AAA GAA GAG CTT GAG CAC GCC TTG AAG GAG CAA GGG TTG TAT GAC
342▶Gly Tyr Ile Thr Lys Glu Glu Leu Glu His Ala Leu Lys Glu Gln Gly Leu Tyr Asp

1083 GCC GAT AAA ATC AAA GAC ATC ATC TCC GAT GCC GAC TCT GAC AAT GAT GGA AGG ATA
361▶Ala Asp Lys Ile Lys Asp Ile Ile Ser Asp Ala Asp Ser Asp Asn Asp Gly Arg Ile

1140 GAT TAT TCA GAG TTT GTG GCG ATG ATG AGG AAA GGG ACG GCT GGT GCC GAG CCA ATG
380▶Asp Tyr Ser Glu Phe Val Ala Met Met Arg Lys Gly Thr Ala Gly Ala Glu Pro Met

1197 AAC ATC AAG AAG AGG CGA GAC ATA GTC CTA TAG TGAAGTGAAGCAGCAAGTGTGTAATGTAATGTG
399▶Asn Ile Lys Lys Arg Arg Asp Ile Val Leu ...

1263 TATAGCAGCTCAAACAAGCAAATTTGTACATCTGTACACAAATGCAATGGGGTTACTTTTGCAAAAAAAAAAAAAAA
                (j)
1340 AAAAAAAAAA
```

US 6,048,695

Fig. 30A

Maize Pollen CDPK cDNA sequence
sequence contained in clones pCIB3168 and pCIB3169

```
1 TG CAG ATC ATG CAC CAC CTC TCC GGC CAG CCC AAC GTG GTG GGC CTC CGC GGC GCG
  1▶Gln Ile Met His His Leu Ser Gly Gln Pro Asn Val Val Gly Leu Arg Gly Ala

57 TAC GAG GAC AAG CAG AGC GTG CAC CTC GTC ATG GAG CTG TGC GCG GGC GGG GAG CTC
19▶Tyr Glu Asp Lys Gln Ser Val His Leu Val Met Glu Leu Cys Ala Gly Gly Glu Leu

                        AvaI
114 TTC GAC CGC ATC ATC GCC CGG GGC CAG TAC ACG GAG CGC GGC GCC GCG GAG CTG CTG
 38▶Phe Asp Arg Ile Ile Ala Arg Gly Gln Tyr Thr Glu Arg Gly Ala Ala Glu Leu Leu

171 CGC GCC ATC GTG CAG ATC GTG CAC ACC TGC CAC TCC ATG GGG GTG ATG CAC CGG GAC
 57▶Arg Ala Ile Val Gln Ile Val His Thr Cys His Ser Met Gly Val Met His Arg Asp

           AvaI
228 ATC AAG CCC GAG AAC TTC CTG CTG CTC AGC AAG GAC GAG GAC GCG CCG CTC AAG GCC
 76▶Ile Lys Pro Glu Asn Phe Leu Leu Leu Ser Lys Asp Glu Asp Ala Pro Leu Lys Ala

285 ACC GAC TTC GGC CTC TCC GTC TTC TTC AAG GAG GGC GAG CTG CTC AGG GAC ATC GTC
 95▶Thr Asp Phe Gly Leu Ser Val Phe Phe Lys Glu Gly Glu Leu Leu Arg Asp Ile Val

                                 AvaI
342 GGC AGC GCC TAC TAC ATC GCG CCC GAG GTG CTC AAG AGG AAG TAC GGC CCG GAG GCC
114▶Gly Ser Ala Tyr Tyr Ile Ala Pro Glu Val Leu Lys Arg Lys Tyr Gly Pro Glu Ala

399 GAC ATC TGG AGC GTC GGC GTC ATG CTC TAC ATC TTC CTC GCC GGC GTG CCT CCC TTC
133▶Asp Ile Trp Ser Val Gly Val Met Leu Tyr Ile Phe Leu Ala Gly Val Pro Pro Phe

456 TGG GCA GAG AAC GAG AAC GGC ATC TTC ACC GCC ATC CTG CGA GGG CAG CTT GAC CTC
152▶Trp Ala Glu Asn Glu Asn Gly Ile Phe Thr Ala Ile Leu Arg Gly Gln Leu Asp Leu

513 TCC AGC GAG CCA TGG CCA CAC ATC TCG CCG GGA GCC AAG GAT CTC GTC AAG AAG ATG
171▶Ser Ser Glu Pro Trp Pro His Ile Ser Pro Gly Ala Lys Asp Leu Val Lys Lys Met

570 CTC AAC ATC AAC CCC AAG GAG CGG CTC ACG GCG TTC CAG GTC CTC AAT CAC CCA TGG
190▶Leu Asn Ile Asn Pro Lys Glu Arg Leu Thr Ala Phe Gln Val Leu Asn His Pro Trp

627 ATC AAA GAA GAC GGA GAC GCG CCT GAC ACG CCG CTT GAC AAC GTT GTT CTC GAC AGG
209▶Ile Lys Glu Asp Gly Asp Ala Pro Asp Thr Pro Leu Asp Asn Val Val Leu Asp Arg

684 CTC AAG CAG TTC AGG GCC ATG AAC CAG TTC AAG AAA GCA GCA TTG AGG ATC ATA GCT
228▶Leu Lys Gln Phe Arg Ala Met Asn Gln Phe Lys Lys Ala Ala Leu Arg Ile Ile Ala

741 GGG TGC CTA TCC GAA GAG GAG ATC ACA GGG CTG AAG GAG ATG TTC AAG AAC ATT GAC
247▶Gly Cys Leu Ser Glu Glu Glu Ile Thr Gly Leu Lys Glu Met Phe Lys Asn Ile Asp

798 AAG GAT AAC AGC GGG ACC ATT ACC CTC GAC GAG CTC AAA CAC GGG TTG GCA AAG CAC
266▶Lys Asp Asn Ser Gly Thr Ile Thr Leu Asp Glu Leu Lys His Gly Leu Ala Lys His

855 GGG CCC AAG CTG TCA GAC AGC GAA ATG GAG AAA CTA ATG GAA GCA GCT GAC GCT GAC
285▶Gly Pro Lys Leu Ser Asp Ser Glu Met Glu Lys Leu Met Glu Ala Ala Asp Ala Asp

                                 EcoRI
912 GGC AAC GGG TTA ATT GAC TAC GAC GAA TTC GTC ACC GCA ACA GTG CAT ATG AAC AAA
304▶Gly Asn Gly Leu Ile Asp Tyr Asp Glu Phe Val Thr Ala Thr Val His Met Asn Lys
```

EP 0 571 427 B1

09884452 - 111201

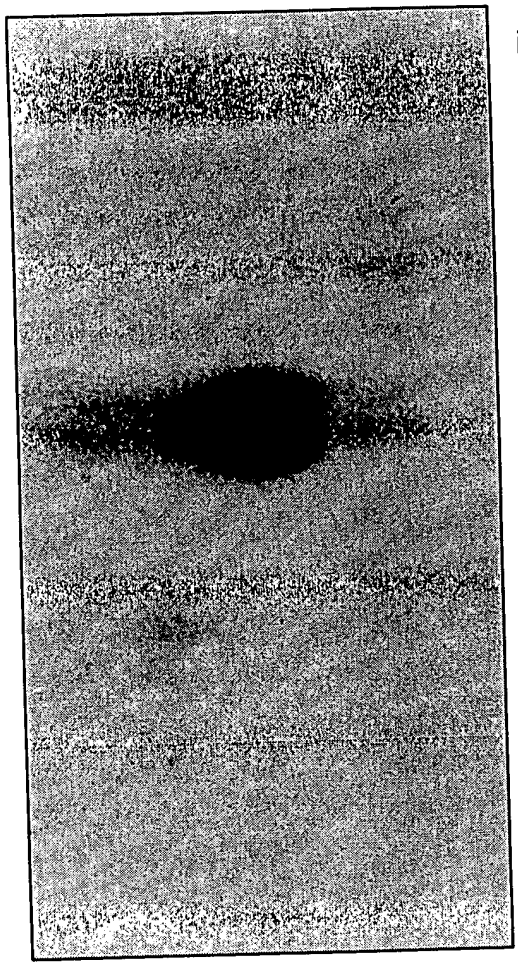


Fig. 31

Fig. 32

Lipman-Pearson Protein Alignment
Gap Penalty: 2; Gap Length Penalty: 12

Seq1	Seq2	Similarity Index	Gap Number	Gap Length	Consensus Length
pol CDPK ptn	rat pk2 ptn				
1>551	1>528	36.5	4	4	297

```
pol CDPK ptn  YSMGKELGRGQFGVTHLCTHRTSGEKLACKTIAKRKLAAREDVDDVRREVQIMHHLSGQPNVVGLRGAYE 162
              Y : .ELG:G.F:V.: C..:TS.:. A K.I..:KL:AR:: :.: RE.:I : L. :PN:V L::: .
rat pk2  ptn  YQLFEELGKGAFSVVRRCVKKTSTQEYAAKIINTKKLSARDH-QKLEREARICRLLK-HPNIVRLHDSIS 81

pol CDPK ptn  DKQSVHLVMELCAGGELFDRIIARGQYTERGAAELLRAIVQIVHTCHSMGVMHRDIKPENFLLLSKDEDA 232
              :.   .LV.:. :GGELF: I:AR. Y:E :A:: ::.I:: V:  H  :::HRD:KPEN:LL SK .:A
rat pk2  ptn  EEGFHYLVFDLVTGGELFEDIVAREYYSEADASHCIHQILESVNHIHQHDIVHRDLKPENLLLASKCKGA 151

pol CDPK ptn  PLKATDFGLSVFFK-EGELLRDIVGSAYYIAPEVL-KRKYGPEADIWSVGVMLYIFLAGVPPFWAENENG 300
              ::K :DFGL::  :..:  : ::.G:: Y::PEVL::. YG  .DIW: GV:LYI:L.G PPFW.E:::
rat pk2  ptn  AVKLADFGLAIEVQGEQQAWFGFAGTPGYLSPEVLRKDPYGKPVDIWACGVILYILLVGYPPFWDEDQHK 221

pol CDPK ptn  IFTAILRGQLDLSSEPWPHISPGAKDLVKKMLNINPKERLTAFQVLNHPWIKEDGDAPDTPLDNVVLDRL 370
              :: .I  G. D::S  W  ::P.AK:L:::ML.INP .R:TA Q.L:HPW: : :..:.    : .:: L
rat pk2  ptn  LYQQIKAGAYDFPSPEWDTVTPEAKNLINQMLTINPAKRITADQALKHPWVCQRSTVASMMHRQETVECL 291

pol CDPK ptn  KQFRAMNQFKKAALRII 387
              ::F.A..::K A L .:
rat pk2  ptn  RKFNARRKLKGAILTTM 308
```

09908462-170204

Fig. 33

Lipman-Pearson Protein Alignment
Gap Penalty: 2; Gap Length Penalty: 12

Seq1	Seq2	Similarity Index	Gap Number	Gap Length	Consensus Length
pol CDPK ptn	humcama ptn				
1>551	1>150	40.3	2	2	142

```
pol CDPK ptn     LSEEEITGLKEMFKNIDKDNSGTITLDELKHGLAKHGPKLSDSEMEKLMEAADADGNGLIDYDEFVTATV 460
                 L:EE:I:.:KE F. :DKD..GTIT .EL   : . G.: :::E::.:::..DADGNG ID: EF:T  .
humcama  ptn     LTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTIDFPEFLTMMA 74

pol CDPK ptn     HMNKL-DREEHLYTAFQYFDKDNSGYITKEELEHALKEQGLYDADKIKDI-ISDADSDNDGRIDYSEFVA 528
                 : M:. D.EE:: .AF: FDKD.:GYI: .EL H.:.: G   ..:.:.::I.:AD D.DG:::Y.EFV.
humcama  ptn     RKMKDTDSEEEIREAFRVKDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEEFVQ 144

pol CDPK ptn     MM 530
                 MM
humcama  ptn     MM 146
```

09508452 - 112201

Fig. 34

Lipman-Pearson Protein Alignment
Gap Penalty: 2; Gap Length Penalty: 12

Seq1	Seq2	Similarity Index	Gap Number	Gap Length	Consensus Length
pol CDPK ptn	soybean CDPK ptn	62.4	1	1	464

```
pol CDPK ptn      VLGRPMEDVRATYSMGKELGRGQFGVTHLCTHRTSGEKLACKTIAKRKLAAREDVDDVRREVQIMHHLSG 150
                  || :. :::|..|.:|:.||:||||.|  ||:|:||.|:|||:|:|||| :|| :||:||:|||||||.
soybean CDPK ptn  VLPQRTQNIREVYEVGRKLGQGQFGTTFECTRRASGGKFACKSIPKRKLLCKEDYEDVWREIQIMHHLSE 91

pol CDPK ptn      QPNVVGLRGAYEDKQSVHLVMELCAGGELFDRIIARGQYTERGAAELLRAIVQIVHTCHSMGVMHRDIKP 220
                  ::||| : |:|||. :||||||||.||||||||:.:|:|:|:|| || |:::||::|::|||:||||||:||
soybean CDPK ptn  HANVVRIEGTYEDSTAVHLVMELCEGGELFDRIVQKGHYSERQAARLIKTIVEVVEACHSLGVMHRDLKP 161

pol CDPK ptn      ENFLLLSKDEDAPLKATDFGLSVFFKEGELLRDIVGSAYYIAPEVLKRKYGPEADIWSVGVMLYIFLAGV 290
                  ||||: : |||| ||||||||||:| || : |:|||:||:||||:: ||||:|:||.||:|||:|:||
soybean CDPK ptn  ENFLFDTIDEDAKLKATDFGLSVFYKPGESFCDVVGSPYYVAPEVLRKLYGPESDVWSAGVILYILLSGV 231

pol CDPK ptn      PPFWAENENGIFTAILRGQLDLSSEPWPHISPGAKDLVKKMLNINPKERLTAFQVLNHPWIKEDGDAPDT 360
                  ||||||:| ||| .|| |:||: ||||| || :|||||:|||: |||.|||| :||.|||| :|. |||.
soybean CDPK      PPFWAESEPGIFRQILLGKLDFHSEPWPSISDSAKDLIRKMLDQNPKTRLTAHEVLRHPWIVDDNIAPDK 301

pol CDPK ptn      PLDNVVLDRLKQFRAMNQFKKAALRIIAGCLSEEEITGLKEMFKNIDKDNSGTITLDELKHGLAKHGPKL 430
                  |||:.||.|||||.|||::|| |||:||. |||||.||||:|| ||.|||||||:||||:|| : |:.|
soybean CDPK ptn  PLDSAVLSRLKQFSAMNKLKKMALRVIAERLSEEEIGGLKELFKMIDTDNSGTITFDELKDGLKRVGSEL 371

pol CDPK ptn      SDSEMEKLMEAADADGNGLIDYDEFVTATVHMNKLDREEHLYTAFQYFDKDNSGYITKEELEHALKEQGL 500
                  :||:..||:||| | :| |||:||::||||:|||:|||:| :|| |||||.||||| :|:::| |: ||
soybean CDPK ptn  MESEIKDLMDAADIDKSGTIDYGEFIAATVHLNKLEREENLVSAFSYFDKDGSGYITLDEIQQACKDFGL 441

pol CDPK ptn      YDADKIKDIISDADSDNDGRIDYSEFVAMMRKGTAGAEPMNIKK  544
                  |. .|.|:|.: | ||||:|||:||.|||||.:| ....::|
soybean CDPK ptn -DDIHIDDMIKEIDQDNDGQIDYGEFAAMMRKGNGGIGRRTMRK  484
```

09538252 - 111203

Fig. 35A

pol CDPK gene Map (1 > 4165) Site and Sequence
Enzymes : 6 of 198 enzymes (Filtered)
Settings : Circular, Certain Sites Only, Standard Genetic Code

TTAGTAACACCTCTCCAATCGCTTGGGTTGGCACATTCTTAGCTTTTATCACATTTTAAGAAATAGAGTTCACCACCTTC 80

AAAATATGCCTATACAATGAATGATGCTTGGATGCAATATAGCTAGATTCAACTAGCTATATATGGTCAATAGAACCCTG 160

TGAGCACCTCACAAACACGACTTCAATTTTGAGACCCTAAGCGAGTAAATGGTTAAAGTCCTCTTATTATTAGTCTTAGG 240

ACTTCTCCTTGCTAAATGCTTGTCAGCGATCTATATATCTTCCCCACTGCGGGAGATACTATATATAGGGCCTTGGACCT 320

CTAGGGTATCTCAAAGGCCTAGTCACAACAATTCTCAACAGTATTTAATTTTATACATGTATGAACAGTGTAGGAATTTG 400

AGTGCCCAACCCAAGAGTGGGAGGTGTAAATTGGGTAGCTAAACTTAAATAGGGCTCTTCTTATTTAGGTTTATCTAGTC 480

TCTACTTAGACTAATTCAGAAAGAATTTTACAACCTATGGTTAATCATATCTCTAGTCTAAGCAAATTTAGGAAAGTTAA 560

AAGCACACAATTAGGCACATGTGAAAGATGTGTATGGTAAGTAAAAGACTTATAAGGAAAAAGTGGGTGAATCCTCAAGA 640

TGTGGTGGTATATCCCAATGATATTAGATGCCAGAATATAGGGGGGAAATCGATGTATACCATCTCTACCAGGATACCTG 720

TGCGGACTGTGCAACTGACACATGGACCATGGTGTCTTCTTAGATTTGGTTATTAGCTAATTGCGCTACAACTTGTTCAA 800

GGCTAGACCAAATTAAAAAACTAATATTAAACATAAAAAGTTAGGCAAACTATAGTAAATTATGCAGCGATCCAACAACA 880

AGCCATGTCTCGTGGGTCATGAGCCACGCGTCGGCCATACACCCACATGATGTTTCCATACGGATGGTCCTTATGCAATT 960

TTGTCTGCAAAACACAAGCCTTAATACAGCCACGCGACAATCATGGAAGTGGTCGTTTTAGGTCCTCATCATGAAGTTCA 1040

GGGAAAACGCATCAAATGTAATGCAGAGAAATGGTATTTCTTCTCTTGTAAATCAGGGAGAGGAGTACCATCAGTACAGA 1120

EcoR I

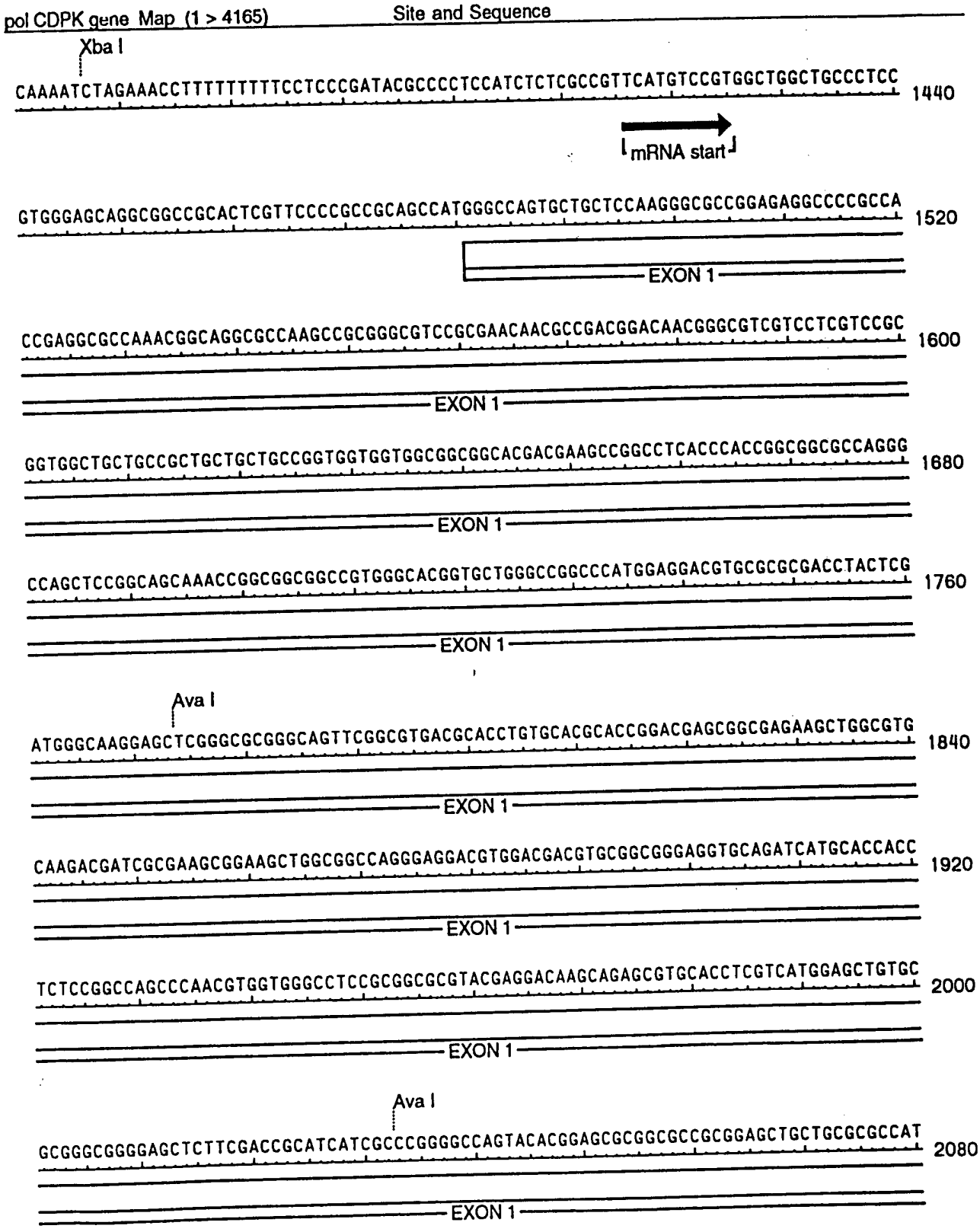
TTCAGAATCAGAATTCAGTCTTCCAACGACAATAATCGCAGCATCTTGTAAAAATTTGCAGAAACTTCTGTTTGACTTGT 1200

AGCCCTGACCTTTGCAAATATTTGAAGTTGTGCCTGCTGACACAACTTCAATCTGGAAGTGCTGTTGATCAGTTTTGCCA 1280

GAAACAGCAAGCAGCCTATATATATCTGTCACGAGACACCCTGCCGCCCTCTTCTTTCCCGCCATTCCCTCCCTACCCTT 1360

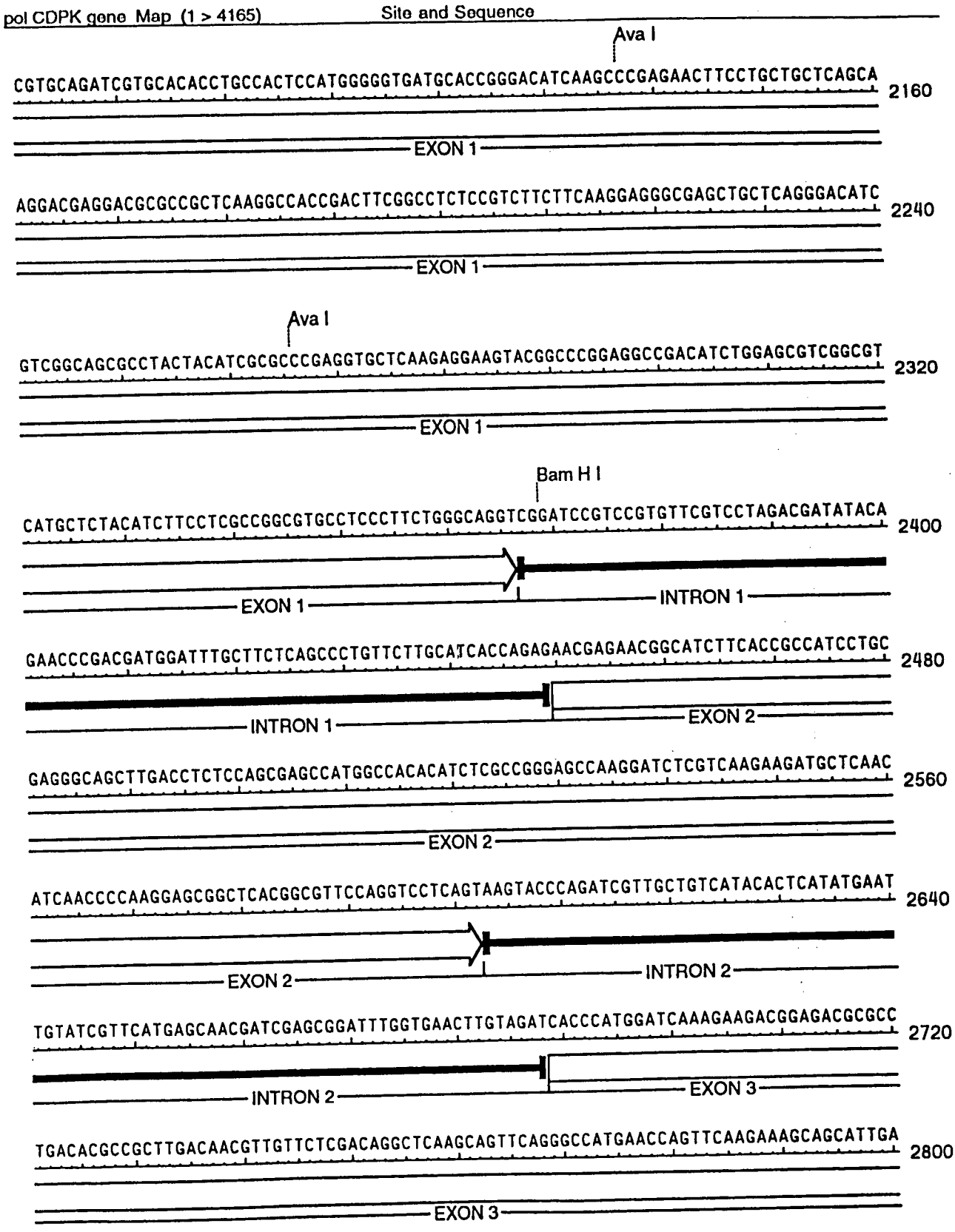
EP 0 921 194 A2

Fig. 35B



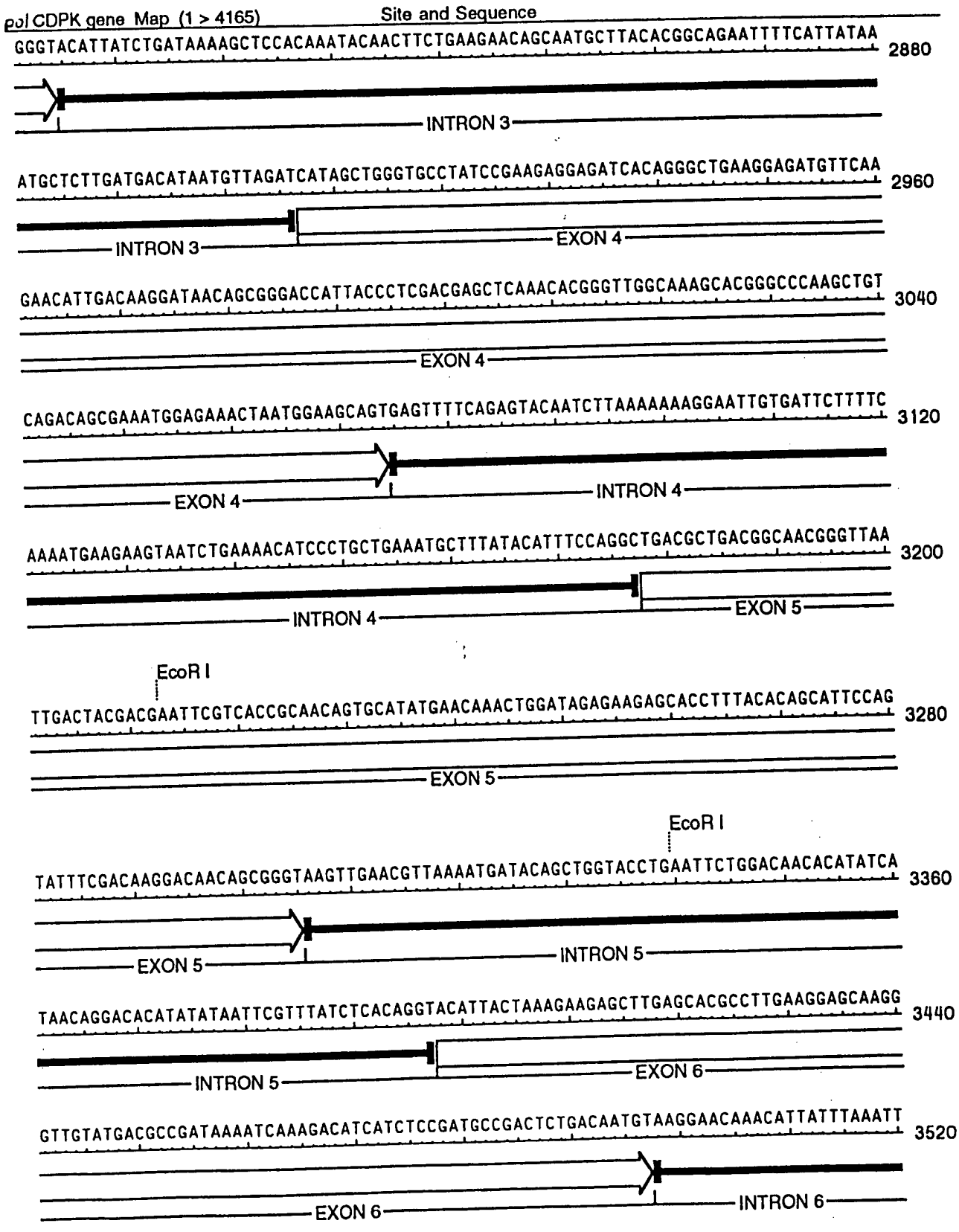
5,968,792 - 4 Oct 99

Fig. 35C



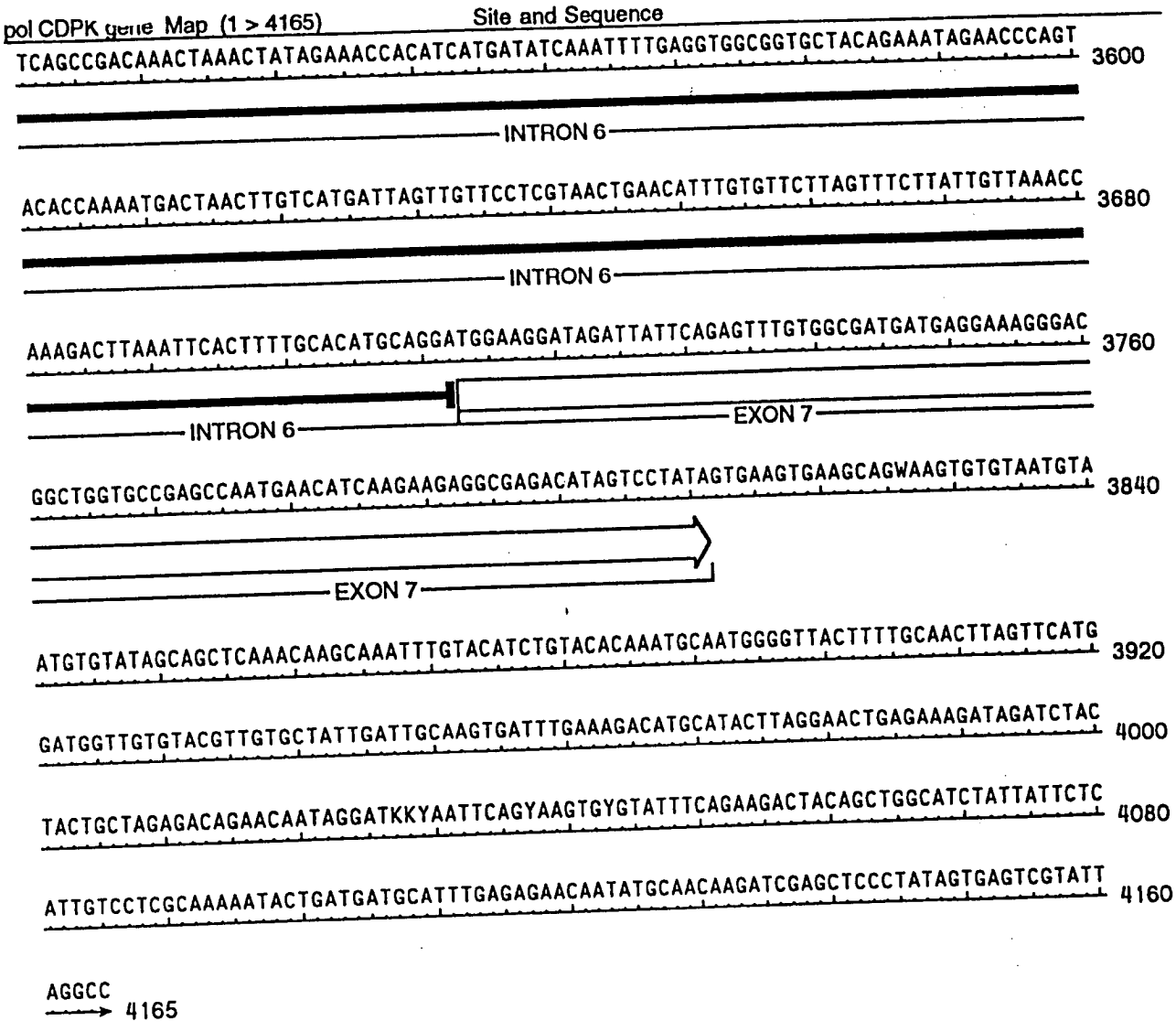
EPO-Patent-0 268 456

Fig. 35D



5,565,428 - 14 - Oct. 15, 1996

Fig. 35E



95984602 - 4-20-04

TOOZTT 29h88660

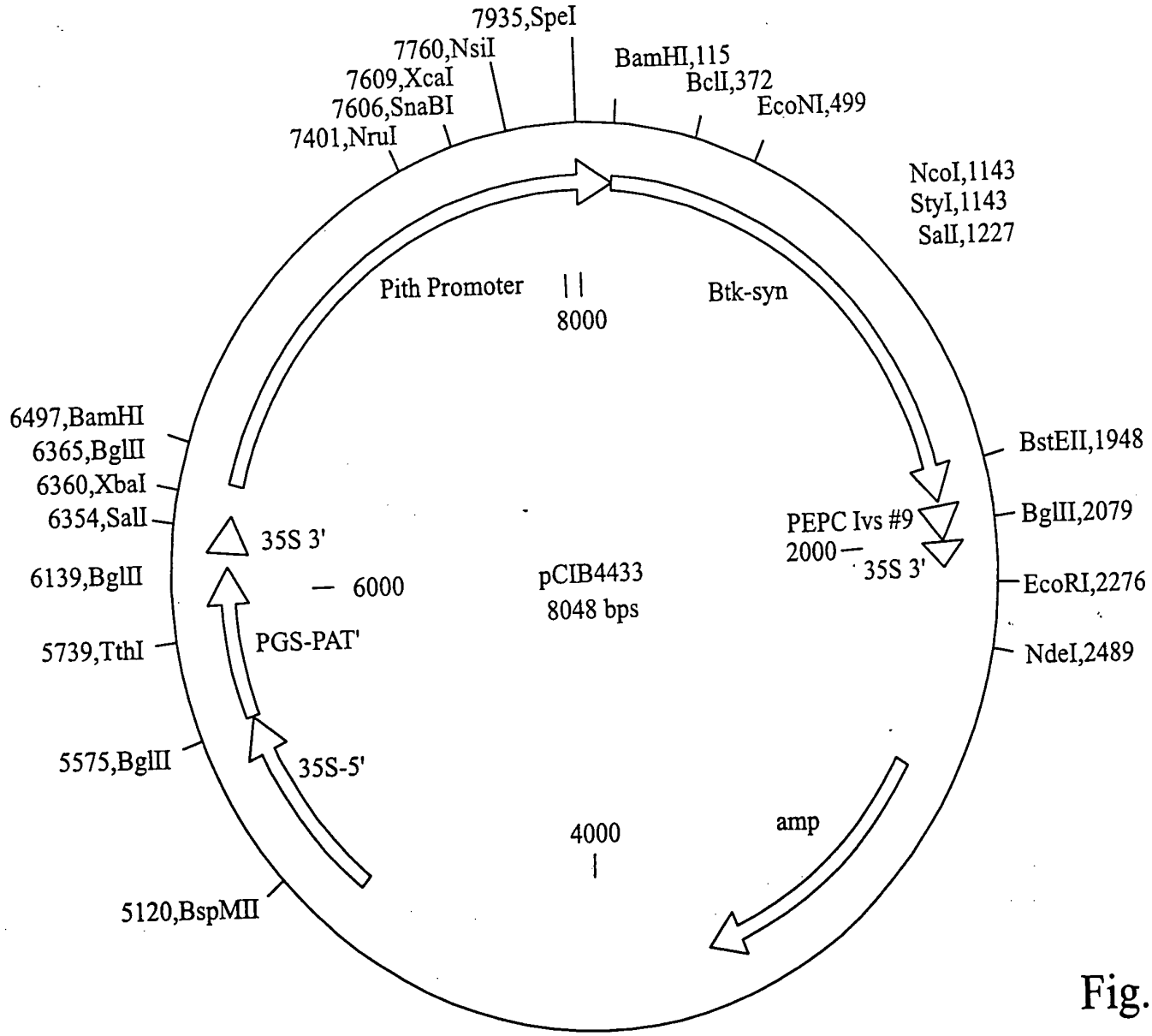


Fig. 36

Fig. 37A

```
   1 ATGGACAACA ACCCCAACAT CAACGAGTGC ATCCCCTACA ACTGCCTGAG CAACCCCGAG
     NetAspAsn AsnProAsn IleAsnGluCys IleProTyr AsnCysLeu SerAsnProGlu

  61 GTGGAGGTGC TGGGCGGCGA GCGCATCGAG ACCGGCTACA CCCCCATCGA CATCAGCCTG
     ValGluVal LeuGlyGly GluArgIleGlu ThrGlyTyr ThrProIle AspIleSerLeu

 121 AGCCTGACCC AGTTCCTGCT GAGCGAGTTC GTGCCCGGCG CCGGCTTCGT GCTGGGCCTG
     SerLeuThr GlnPheLeu LeuSerGluPhe ValProGly AlaGlyPhe ValLeuGlyLeu

 181 GTGGACATCA TCTGGGGCAT CTTCGGCCCC AGCCAGTGGG ACGCCTTCCT GGTGCAGATC
     ValAspIle IleTrpGly IlePheGlyPro SerGlnTrp AspAlaPhe LeuValGlnIle

 241 GAGCAGCTGA TCAACCAGCG CATCGAGGAG TTCGCCCGCA ACCAGGCCAT CAGCCGCCTG
     GluGlnLeu IleAsnGln ArgIleGluGlu PheAlaArg AsnGlnAla IleSerArgLeu

 301 GAGGGCCTGA GCAACCTGTA CCAAATCTAC GCCGAGAGCT TCCGCGAGTG GGAGGCCGAC
     GluGlyLeu SerAsnLeu TyrGlnIleTyr AlaGluSer PheArgGlu TrpGluAlaAsp

 361 CCCACCAACC CCGCCCTGCG CGAGGAGATG CGCATCCAGT TCAACGACAT GAACAGCGCC
     ProThrAsn ProAlaLeu ArgGluGluMet ArgIleGln PheAsnAsp MetAsnSerAla

 421 CTGACCACCG CCATCCCCCT GTTCGCCGTG CAGAACTACC AGGTGCCCCT GCTGAGCGTG
     LeuThrThr AlaIlePro LeuPheAlaVal GlnAsnTyr GlnValPro LeuLeuSerVal

 481 TACGTGCAGG CCGCCAACCT GCACCTGAGC GTGCTGCGCG ACGTCAGCGT GTTCGGCCAG
     TyrValGln AlaAlaAsn LeuHisLeuSer ValLeuArg AspValSer ValPheGlyGln

 541 CGCTGGGGCT TCGACGCCGC CACCATCAAC AGCCGCTACA ACGACCTGAC CCGCCTGATC
     ArgTrpGly PheAspAla AlaThrIleAsn SerArgTyr AsnAspLeu ThrArgLeuIle

 601 GGCAACTACA CCGACCACGC CGTGCGCTGG TACAACACCG GCCTGGAGCG CGTGTGGGGT
     GlyAsnTyr ThrAspHis AlaValArgTrp TyrAsnThr GlyLeuGlu ArgValTrpGly

 661 CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTG
     ProAspSer ArgAspTrp IleArgTyrAsn GlnPheArg ArgGluLeu ThrLeuThrVal

 721 CTGGACATCG TGAGCCTGTT CCCCAACTAC GACAGCCGCA CCTACCCCAT CCGCACCGTG
     LeuAspIle ValSerLeu PheProAsnTyr AspSerArg ThrTyrPro IleArgThrVal

 781 AGCCAGCTGA CCCGCGAGAT TTACACCAAC CCCGTGCTGG AGAACTTCGA CGGCAGCTTC
     SerGlnLeu ThrArgGlu IleTyrThrAsn ProValLeu GluAsnPhe AspGlySerPhe

 841 CGCGGCAGCG CCCAGGGCAT CGAGGGCAGC ATCCGCAGCC CCCACCTGAT GGACATCCTG
     ArgGlySer AlaGlnGly IleGluGlySer IleArgSer ProHisLeu MetAspIleLeu

 901 AACAGCATCA CCATCTACAC CGACGCCCAC CGCGGCGAGT ACTACTGGAG CGGCCACCAG
     AsnSerIle ThrIleTyr ThrAspAlaHis ArgGlyGlu TyrTyrTrp SerGlyHisGln

 961 ATCATGGCCA GCCCCGTCGG CTTCAGCGGC CCCGAGTTCA CCTTCCCCCT GTACGGCACC
     IleMetAla SerProVal GlyPheSerGly ProGluPhe ThrPhePro LeuTyrGlyThr

1021 ATGGGCAACG CTGCACCTCA GCAGCGCATC GTGGCACAGC TGGGCCAGGG AGTGTACCGC
     MetGlyAsn AlaAlaPro GlnGlnArgIle ValAlaGln LeuGlyGln GlyValTyrArg

1081 ACCCTGAGCA GCACCCTGTA CCGTCGACCT TTCAACATCG GCATCAACAA CCAGCAGCTG
     ThrLeuSer SerThrLeu TyrArgArgPro PheAsnIle GlyIleAsn AsnGlnGlnLeu

1141 AGCGTGCTGG ACGGCACCGA GTTCGCCTAC GGCACCAGCA GCAACCTGCC CAGCGCCGTG
     SerValLeu AspGlyThr GluPheAlaTyr GlyThrSer SerAsnLeu ProSerAlaVal

1201 TACCGCAAGA GCGGCACCGT GGACAGCCTG GACGAGATCC CCCCTCAGAA CAACAACGTG
     TyrArgLys SerGlyThr ValAspSerLeu AspGluIle ProProGln AsnAsnAsnVal
```

D50884 - 4 5 0 2

EP0574936A2

Fig. 37B

```
1261 CCACCTCGAC AGGGCTTCAG CCACCGTCTG AGCCACGTGA CCATGTTCCG CAGTGGCTTC
     ProProArg GlnGlyPhe SerHisArgLeu SerHisVal SerMetPhe ArgSerGlyPhe

1321 AGCAACAGCA GCGTGAGCAT CATCCGTGCA CCTATGTTCA GCTGGATTCA CCGCAGTGCC
     SerAsnSer SerValSer IleIleArgAla ProMetPhe SerTrpIle HisArgSerAla

1381 GAGTTCAACA ACATCATCCC CAGCAGCCAG ATCACCCAGA TCCCCCTGAC CAAGAGCACC
     GluPheAsn AsnIleIle ProSerSerGln IleThrGln IleProLeu ThrLysSerThr

1441 AACCTGGGCA GCGGCACCAG CGTGGTGAAG GGCCCCGGCT TCACCGGCGG CGACATCCTG
     AsnLeuGly SerGlyThr SerValValLys GlyProGly PheThrGly GlyAspIleLeu

1501 CGCCGCACCA GCCCCGGCCA GATCAGCACC CTGCGCGTGA ACATCACCGC CCCCCTGAGC
     ArgArgThr SerProGly GlnIleSerThr LeuArgVal AsnIleThr AlaProLeuSer

1561 CAGCGCTACC GCGTCCGCAT CCGCTACGCC AGCACCACCA ACCTGCAGTT CCACACCAGC
     GlnArgTyr ArgValArg IleArgTyrAla SerThrThr AsnLeuGln PheHisThrSer

1621 ATCGACGGCC GCCCCATCAA CCAGGGCAAC TTCAGCGCCA CCATGAGCAG CGGCAGCAAC
     IleAspGly ArgProIle AsnGlnGlyAsn PheSerAla ThrMetSer SerGlySerAsn

1681 CTGCAGAGCG GCAGCTTCCG CACCGTGGGC TTCACCACCC CCTTCAACTT CAGCAACGGC
     LeuGlnSer GlySerPhe ArgThrValGly PheThrThr ProPheAsn PheSerAsnGly

1741 AGCAGCGTGT TCACCCTGAG CGCCCACGTG TTCAACAGCG GCAACGAGGT GTACATCGAC
     SerSerVal PheThrLeu SerAlaHisVal PheAsnSer GlyAsnGlu ValTyrIleAsp

1801 CGCATCGAGT TCGTGCCCGC CGAGGTGACC TTCGAGGCCG AGTACGACCT GGAGAGGGCT
     ArgIleGlu PheValPro AlaGluValThr PheGluAla GluTyrAsp LeuGluArgAla

1861 CAGAAGGCCG TGAACGAGCT GTTCACCAGC AGCAACCAGA TCGGCCTGAA GACCGACGTG
     GlnLysAla ValAsnGlu LeuPheThrSer SerAsnGln IleGlyLeu LysThrAspVal

1921 ACCGACTACC ACATCGATCA AGTATCCAAT TTAGTTGAGT GTTTATCTGA TGAATTTTGT
     ThrAspTyr HisIleAsp GlnValSerAsn LeuValGlu CysLeuSer AspGluPheCys

1981 CTGGATGAAA AAAAAGAATT GTCCGAGAAA GTCAAACATG CGAAGCGACT TAGTGATGAG
     LeuAspGlu LysLysGlu LeuSerGluLys ValLysHis AlaLysArg LeuSerAspGlu

2041 CGGAATTTAC TTCAAGATCC AAACTTTAGA GGGATCAATA GACAACTAGA CCGTGGCTGG
     ArgAsnLeu LeuGlnAsp ProAsnPheArg GlyIleAsn ArgGlnLeu AspArgGlyTrp

2101 AGAGGAAGTA CGGATATTAC CATCCAAGGA GGCGATGACG TATTCAAAGA GAATTACGTT
     ArgGlySer ThrAspIle ThrIleGlnGly GlyAspAsp ValPheLys GluAsnTyrVal

2161 ACGCTATTGG GTACCTTTGA TGAGTGCTAT CCAACGTATT TATATCAAAA AATAGATGAG
     ThrLeuLeu GlyThrPhe AspGluCysTyr ProThrTyr LeuTyrGln LysIleAspGlu

2221 TCGAAATTAA AAGCCTATAC CCGTTACCAA TTAAGAGGGT ATATCGAAGA TAGTCAAGAC
     SerLysLeu LysAlaTyr ThrArgTyrGln LeuArgGly TyrIleGlu AspSerGlnAsp

2281 TTAGAAATCT ATTTAATTCG CTACAATGCC AAACACGAAA CAGTAAATGT GCCAGGTACG
     LeuGluIle TyrLeuIle ArgTyrAsnAla LysHisGlu ThrValAsn ValProGlyThr

2341 GGTTCCTTAT GGCCGCTTTC AGCCCCAAGT CCAATCGGAA AATGTGGGGA GCCGAATCGA
     GlySerLeu TrpProLeu SerAlaProSer ProIleGly LysCysGly GluProAsnArg

2401 TGCGCTCCGC ACCTGGAGTG GAACCCGGAC CTAGACTGCA GCTGCAGGGA CGGGGAGAAG
     CysAlaPro HisLeuGlu TrpAsnProAsp LeuAspCys SerCysArg AspGlyGluLys

2461 TGCGCCCATC ATTCCCATCA TTTCTCCTTG GACATTGATG TTGGATGTAC AGACTTAAAT
     CysAlaHis HisSerHis HisPheSerLeu AspIleAsp ValGlyCys ThrAspLeuAsn

2521 GAGGACTTAG GTGTATGGGT GATATTCAAG ATTAAGACGC AAGATGGCCA TGCAAGACTA
     GluAspLeu GlyValTrp ValIlePheLys IleLysThr GlnAspGly HisAlaArgLeu

2581 GGAAATCTAG AATTTCTCGA AGAGAAACCA TTAGTAGGAG AAGCACTAGC TCGTGTGAAA
     GlyAsnLeu GluPheLeu GluGluLysPro LeuValGly GluAlaLeu AlaArgValLys
```

Fig. 37C

```
2641 AGAGCGGAGA 2VGWkTGGAG AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATTGTT
     ArgAlaGlu LysLysTrp ArgAspLysArg GluLysLeu GluTrpGlu ThrAsnIleVal

2701 TATAAAGAGG CAAAAGAATC TGTAGATGCT TTATTTGTAA ACTCTCAATA TGATAGATTA
     TyrLysGlu AlaLysGlu SerValAspAla LeuPheVal AsnSerGln TyrAspArgLeu

2761 CAAGCGGATA CCAACATCGC GATGATTCAT GCGGCAGATA AACGCGTTCA TAGCATTCGA
     GlnAlaAsp ThrAsnIle AlaMetIleHis AlaAlaAsp LysArgVal HisSerIleArg

2821 GAAGCTTATC TGCCTGAGCT GTCTGTGATT CCGGGTGTCA ATGCGGCTAT TTTTGAAGAA
     GluAlaTyr LeuProGlu LeuSerValIle ProGlyVal AsnAlaAla IlePheGluGlu

2881 TTAGAAGGGC GTATTTTCAC TGCATTCTCC CTATATGATG CGAGAAATGT CATTAAAAAT
     LeuGluGly ArgIlePhe ThrAlaPheSer LeuTyrAsp AlaArgAsn ValIleLysAsn

2941 GGTGATTTTA ATAATGGCTT ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA
     GlyAspPhe AsnAsnGly LeuSerCysTrp AsnValLys GlyHisVal AspValGluGlu

3001 CAAAACAACC ACCGTTCGGT CCTTGTTGTT CCGGAATGGG AAGCAGAAGT GTCACAAGAA
     GlnAsnAsn HisArgSer ValLeuValVal ProGluTrp GluAlaGlu ValSerGlnGlu

3061 GTTCGTGTCT GTCCGGGTCG TGGCTATATC CTTCGTGTCA CAGCGTACAA GGAGGGATAT
     ValArgVal CysProGly ArgGlyTyrIle LeuArgVal ThrAlaTyr LysGluGlyTyr

3121 GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAATA CAGACGAACT GAAGTTTAGC
     GlyGluGly CysValThr IleHisGluIle GluAsnAsn ThrAspGlu LeuLysPheSer

3181 AACTGTGTAG AAGAGGAAGT ATATCCAAAC AACACGGTAA CGTGTAATGA TTATACTGCG
     AsnCysVal GluGluGlu ValTyrProAsn AsnThrVal ThrCysAsn AspTyrThrAla

3241 ACTCAAGAAG AATATGAGGG TACGTACACT TCTCGTAATC GAGGATATGA CGGAGCCTAT
     ThrGlnGlu GluTyrGlu GlyThrTyrThr SerArgAsn ArgGlyTyr AspGlyAlaTyr

3301 GAAAGCAATT CTTCTGTACC AGCTGATTAT GCATCAGCCT ATGAAGAAAA AGCATATACA
     GluSerAsn SerSerVal ProAlaAspTyr AlaSerAla TyrGluGlu LysAlaTyrThr

3361 GATGGACGAA GAGACAATCC TTGTGAATCT AACAGAGGAT ATGGGGATTA CACACCACTA
     AspGlyArg ArgAspAsn ProCysGluSer AsnArgGly TyrGlyAsp TyrThrProLeu

3421 CCAGCTGGCT ATGTGACAAA AGAATTAGAG TACTTCCCAG AAACCGATAA GGTATGGATT
     ProAlaGly TyrValThr LysGluLeuGlu TyrPhePro GluThrAsp LysValTrpIle

3481 GAGATCGGAG AAACGGAAGG AACATTCATC GTGGACAGCG TGGAATTACT TCTTATGGAG
     GluIleGly GluThrGlu GlyThrPheIle ValAspSer ValGluLeu LeuLeuMetGlu

3541 GAATAA
     Glu---
```

Fig37C-2964866

T0227T 29h88660

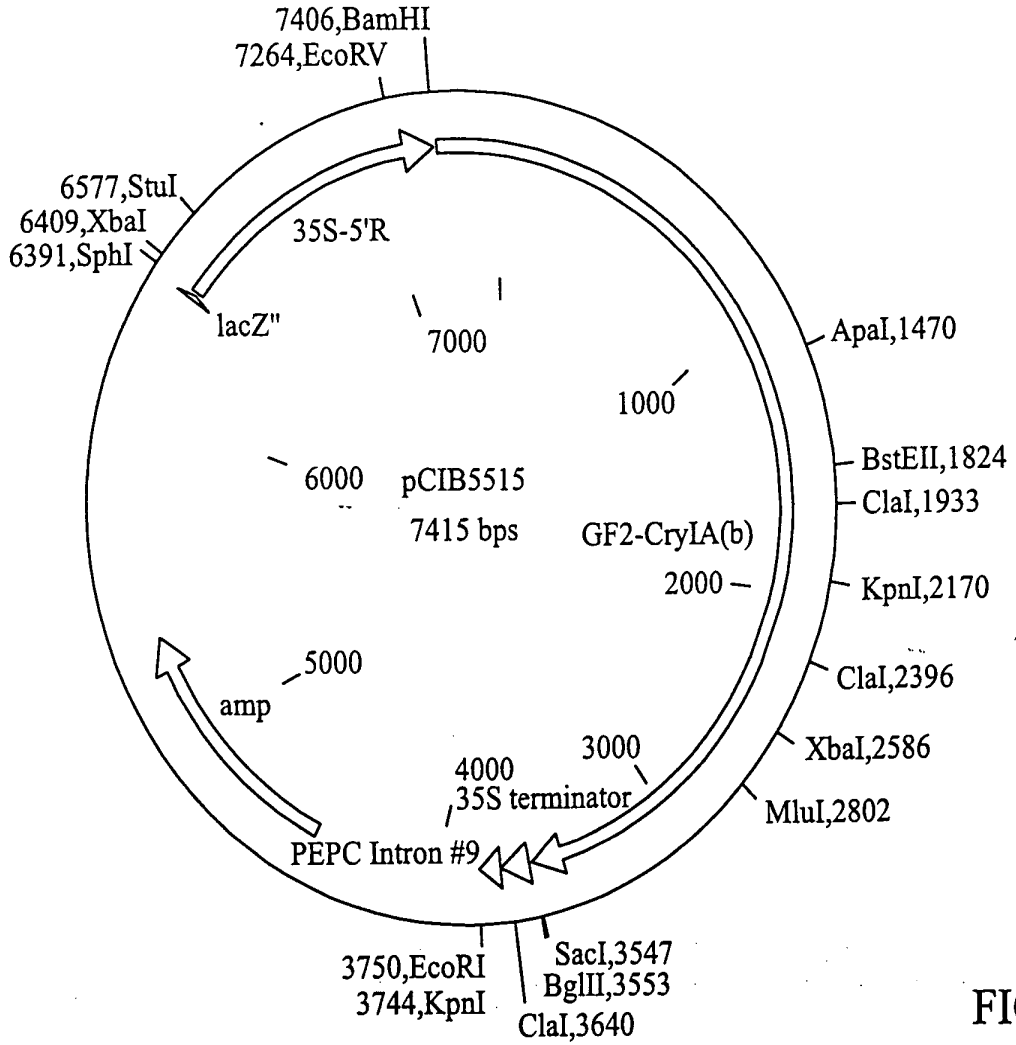


FIG. 38